

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2000, 17:16:18 : Search time 937.26 Seconds
(without alignments)
2194.834 Million cell updates/sec

Title: US-09-050-249-1
Perfect score: 471
Sequence: 1 AACCTTGCGCAGCTTCACTG.....TCACCTACTACATCAAGT 471

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1034670 seqs, 2183789903 residues
Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBml: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_om: *
4: gb_ov: *
5: gb_pat: *
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7: gb_pl1: *
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94: gb_vl2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470.6	99.9	471	5	AR072044
2	470.6	99.9	471	5	E13264 Mouse cDNA
3	470.6	99.9	471	5	E14257 CDNA encodi
4	470.6	99.9	471	5	E14760 CDNA encodi
5	470.6	99.9	471	5	E17139 Murine mRNA
6	470.6	99.9	471	22	E10609 Mouse cDNA
7	470.6	99.9	471	22	E11744 CDNA encodi
8	470.6	99.9	471	22	E12010 CDNA encodi
9	470.6	99.9	866	12	MUSIGIFP
10	452	96.0	572	12	MMU66244 Mus musculi
11	400.6	85.1	722	12	RNU77776 Rattus norv
12	395.8	84.0	628	12	RNAJ813 Rattus no

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13 392.4 83.3 483 12 RN13337 Y13337 Rattus norv
14 279.8 59.4 665 12 RN07777 U77777 Rattus norv
15 279.2 59.3 471 13 ASIGIF Y09278 Attifical
16 268.4 57.0 582 3 ECIGIF Y11311 Equus caball
17 254 53.9 534 3 AF13175 AF13175 Bos tauru
18 254 53.9 754 3 AF124789 AF124789 Bos tauru
19 247.8 52.6 471 5 E17135 E17135 Human mRN
20 247.8 52.6 579 66 HSU90434 U90434 Human inter
21 247.8 52.6 1102 35 D49950 D49950 Homo sapien
22 247.4 52.5 471 5 E13263 E13263 Human cDNA
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24 247.4 52.5 471 22 E12009 E12009 cDNA encodi
25 247.4 52.5 579 3 AR069452 AR069452 Sequence
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27 247.4 52.5 1120 5 E14759 E14759 cDNA encodi
28 247.4 52.5 1120 5 E15641 E15641 Human mRN
29 247.4 52.5 1120 22 E11745 E11745 cDNA encodi
30 247 52.4 589 11 AF077611 AF077611 Homo sapi
31 244.6 51.9 471 5 E17136 E17136 IGIF/MUT35
32 244.4 51.9 579 3 AF191088 AF191088 Sus scrofa
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34 244.4 51.9 582 3 CFIGIF Y11133 Canis famli
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36 244.4 51.9 665 3 AB010003 AB010003 Sus scrofa
37 243 51.6 471 5 E17137 E17137 IGIF/MUT42
38 242.2 51.4 600 3 AF176949 AF176949 Sus scrofa
39 225 47.8 110931 79 AC027079 AC027079 Mus muscu
40 127.8 27.1 11464 5 E15652 E15652 Human gene
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ALIGNMENTS

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RESULT 1
LOCUS AR072044 471 bp DNA PAT 18-FEB-2000
DEFINITION Sequence 1 from patent US 5912324.
ACCESSION AR072044
VERSION AR072044.1 GI:7222932
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 471)
AUTHORS Kohno,K., Tanimoto,T., Torigoe,K., Kunikata,T., Taniguchi,M.,
TITLE Interferon-gamma (IFN-gamma.) Inducing factor (IGIF, IL-18)
JOURNAL Patent: US 5912324-A 1 15-JUN-1999;
FEATURES
SOURCE Location/Qualifiers
1..471
BASE COUNT 162 a 91 c 92 g 125 t 1 others
ORIGIN

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Query Match 99.9%; Score 470.6; DB 5; Length 471;
 Best Local Similarity 100.0%; Pred. No. 1.3e-103;
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AACTTGGCCACTTCATGTACCAACCCAGTATACGGAATATTAATGACCAAGTCTC 60
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Db 1 AACTTGGCCACTTCATGTACCAACCCAGTATACGGAATATTAATGACCAAGTCTC 60
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QY 61 TTGCTTGACAAAGACACCGCTGTGTCGAGATATGACTGATTTGATCAAGTCCAGT 120
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Db 61 TTGCTTGACAAAGACACCGCTGTGTCGAGATATGACTGATTTGATCAAGTCCAGT 120
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Db 421 GAAATGGGATTAATCTGTAATGTTTCACTCTCACTTACATCAATCAAGT 471
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RESULT 2
LOCUS E13264 471 bp DNA PAT 24-JUN-1998
DEFINITION Mouse cDNA encoding a protein that induces to produce
ACCESSION E13264
VERSION E13264.1 GI:3252069
KEYWORDS JP 1997157180-A/2.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 471)
AUTHORS Torigoe,K., Tanimoto,T., Fukuda,S. and Kurimoto,M.
TITLE AGENT FOR SENSITIVE DISEASE
JOURNAL Patent: JP 1997157180-A 2 17-JUN-1997;
COMMENT HAYASHIBARA BIOCHEM LAB INC
OS Mus sp. (mouse)
PN JP 1997157180-A/2
PD 17-JUN-1997
PR 24-JAN-1996 JP 1996028722
PR 10-MAR-1995 JP 95P 279906
PI TORIGOE RAKUJI, TANIMOTO TADAO, FUKUDA SHIGETSU, PI
KURIMOTO MASASHI
PC A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,C07K14/52;
PC C07K14/54;
PC C07K14/55;
CC strandedness: Double;
CC topology: Linear;
CC Feature is identified by similarity;
FH Key Location/Qualifiers
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FT mat-peptide 1..471
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FT Location/Qualifiers
1..471
/db_xref="taxon:10095"

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Query Match 99.9%; Score 470.6; DB 5; Length 471;
 Best Local Similarity 100.0%; Pred. No. 1.3e-103;
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TTGCTTGACAAAGACACCGCTGTGTCGAGATATGACTGATTTGATCAAGTCCAGT 120
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Matches	471: Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	1 AACTTTGGCCGACTTCTACTGTACAAACCCAGATATACGATATATAATGACCAAGTTCTC	60
Y	61 TTGCTTGACAAAGACAGCGCTGTGTCGAGATATAGCATATATGATCAAGTCCAGT	120
Db	61 TTGCTTGACAAAGACAGCGCTGTGTCGAGATATAGCATATATGATCAAGTCCAGT	120
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Db	361 CACTTTCTTCTGCTTGCACAAAGAGATGATGCTTTCAACATCATTTCTGAAAAAAGAT	420
Y	421 GAAATGGGGATTAATCTGTATCTTCACTCTCCACTACTACTTCAATCAAGT	471
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RESULT	4	
LOCUS	E14760	471 bp DNA 28-JUL-1999
DEFINITION	cDNA encoding polypeptide which induces interferon-gamma production	
ACCESSION	E14760	
VERSION	E14760.1	GI:5709443
KEYWORDS	JP 1998007699-A/2.	
SOURCE	Mus sp.	
ORGANISM	Mus sp.	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
AUTHORS	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE	1 (bases 1 to 471)	
JOURNAL	Ushio, S., Toriige, K., Tanimoto, T., Okamura, H. and Kurimoto, M.	
COMMENT	POLYPEPTIDE INDUCING PRODUCTION OF INTERFERON-GAMMA	
	Patent: JP 1998007699-A 13-JAN-1998;	
	HAYASHIBARA BIOCHEM LAB INC	
	OS Mus sp. (mouse)	
	PN JP 1998007699-A/2	
	PD 13-JAN-1998	
	PF 18-SEP-1995 JP 1997058547	
	PR 15-NOV-1994 JP 94P 304203	
	PI USHIO SHINPEI, TORIIGE KAKUYI, TANIMOTO TADAO, OKAMURA HARUKI,	
	PI KURIMOTO MASASHI	
	PC C07K4/52, C07H21/04, C12N1/21, C12N15/09, C12P21/02, /A61K38/00,	
	PC (C12N1/21), (C12P21/02), (C12N1/19);	

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CC      topology: Linear;
CC      hypothetical: No;
CC      anti-sense: No;
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FT      /organism="Mus sp."
FT      /tissue_type="liver"
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Best Local Similarity 100.0%; Pred. No. 1.3e-103;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACCTTGGCCGACTTCTACTGTACAAACCGCAGTAATACGGAATATAATGACCAGTTCTC 60
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QY      61 TTCGTTGACAAAGACAGCCTGTGTTCCGAGATATGACTGATATGATCAAGTCCAGT 120
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QY      361 CACTTTCTTCTTGGCCAAAAGAGATGATGCTTTCAACTCATTTCTGAAAAAAGAGAT 420
Db      361 CACTTTCTTCTTGGCCAAAAGAGATGATGCTTTCAACTCATTTCTGAAAAAAGAGAT 420
QY      421 GAAATGGGGATAATCTGTAATGTTCACTCTCACTACTACTACATCAAGT 471
Db      421 GAAATGGGGATAATCTGTAATGTTCACTCTCACTACTACTACTACATCAAGT 471

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LOCUS      Murine mRNA for Interleukin-18 (IL-18).
ACCESSION      E17139
VERSION      E17139.1 GI:5711822
KEYWORDS      JP 1998236974-A/5.
SOURCE      Mus sp.
ORGANISM      Mus sp.
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 471)
AUTHORS      Matthew T.G., Nicholl J.H., Udagawa N. and Kurimoto M.
TITLE      OSTEOCLAST-FORMATION INHIBITOR
JOURNAL      Patent: JP 1998236974-A 08-SEP-1998;
HAYASHIBARA BIOCHEM LAB INC
COMMENT      OS Mus sp. (mouse)
PN JP 1998236974-A/5
PD 08-SEP-1998

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PF      25-FEB-1997 JP 1997055468
PI      MATTHEW TODD GALSPIE, NICHOLL JOY HOOWOOD, UDAGAWA NOBUYUKI,
PI      KURIMOTO MASASHI
PC      A61K38/00,A61K38/00//C07K14/54,C12N15/09;
CC      strandedness: Double;
CC      topology: Linear;
FH      Key      Location/Qualifiers
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Best Local Similarity 99.8%; Pred. No. 1.3e-103;
Matches 470; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACCTTGGCCGACTTCTACTGTACAAACCGCAGTAATACGGAATATAATGACCAGTTCTC 60
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QY      61 TTCGTTGACAAAGACAGCCTGTGTTCCGAGATATGACTGATATGATCAAGTCCAGT 120
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AC      E10609;
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SV      E10609.1
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DT      08-OCT-1997 (Rel. 52, Created)
DD      08-OCT-1997 (Rel. 52, Last updated, Version 1)
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DE      Mouse cDNA encoding a protein involved in interferon-gamma production.
XX
KW      JP 1996027189-A/1.
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OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP 1-471
RA Okamura H., Tanimoto T., Torigoe K., Kurimoto M.;
RT "PROTEIN INDUCING PRODUCTION OF INTERFERON-GAMMA";
RL Patent number JP 1996027189-A/1, 30-JAN-1996.
XX HAYASHIBARA BIOCHEM LAB INC.

OS Mus sp. (mouse)
CC PN JP 1996027189-A/1
CC PD 30-JAN-1996
CC PF 14-JUL-1994 JP 1994184162
CC PI OKAMURA HARUKI, TANIMOTO TADAO, TORIGOE KAKUJI,
CC PC C07K14/52, A61K38/00, A61K38/00, C12N1/21, C12N15/09,
CC PC C12P21/02, C07K14/57;
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CC CC topology: Linear;
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Sequence 471 BP; 162 A; 91 C; 92 G; 125 T; 1 other;

Query Match 99.9%; Score 470.6; DB 22; Length 471;
Best Local Similarity 100.0%; Pred. No. 1.3e-103;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DE 08-OCT-1997 (Rel. 52, Last updated, Version 1)
DE CDNA encoding polypeptide which induce mouse interferon-gamma product.
XX JP 1996193098-A/1.
XX Mus musculus (house mouse)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]
RP 1-471
RA Ushio S., Torigoe K., Tanimoto T., Okamura H., Kurimoto M.;
RT "POLYPEPTIDE FOR INDUCING PRODUCTION OF INTERFERON-GAMMA";
RL Patent number JP 1996193098-A/1, 30-JUL-1996.
XX HAYASHIBARA BIOCHEM LAB INC.

OS Mus musculus (mouse)
CC PN JP 1996193098-A/1
CC PD 30-JUL-1996
CC PF 18-SEP-1995 JP 1995262062
CC PR 15-NOV-1994 JP 94P 304203
CC PI USHIO SHINPEI, TORIGOE KAKUJI, TANIMOTO TADAO, OKAMURA HARUKI,
CC PI KURIMOTO MASASHI
CC PC C07K14/52, C07H21/04, C12N1/21, C12N15/09, C12P21/00, A61K38/00,
CC PC C07K14/06,
CC PC C07K7/08, (C12N1/21, C12R1.19), (C12P21/00, C12R1.19);
CC CC strandedness: Double;
CC CC topology: Linear;
CC CC hypothetical: No;
CC CC anti-sense: No;
CC FH key Location/Qualifiers
CC FH source 1.471
CC FT /organism="Mus musculus"
CC FT /tissue_type="liver"
CC FT

Key Location/Qualifiers
FH source 1.471
FH FT /db_xref="taxon:10090"
FH FT /organism="Mus musculus"
FH FT

Sequence 471 BP; 162 A; 91 C; 92 G; 125 T; 1 other;

Query Match 99.9%; Score 470.6; DB 22; Length 471;
Best Local Similarity 100.0%; Pred. No. 1.3e-103;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTGGCCGACTTACCTGATACACCGGAGTATACGATATTAATGACCAAGTCTC 60
DB 1 AACTTGGCCGACTTACCTGATACACCGGAGTATACGATATTAATGACCAAGTCTC 60
QY 61 TTGCTTGACAAAAGACAGCCTGTGTTCGAGATATGATGATATGATCAAGTGCAGT 120
DB 61 TTGCTTGACAAAAGACAGCCTGTGTTCGAGATATGATGATATGATCAAGTGCAGT 120
QY 121 GAACCCAGACAGACTGATATATACATGTACAAAGACAGTGAAGTGAAGTGCCT 180
DB 121 GAACCCAGACAGACTGATATATACATGTACAAAGACAGTGAAGTGAAGTGCCT 180

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Db      121 GAACCCAGACAGCTGATATATATACATGACAAAGACAGTGAAGAGACTGCT 180
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Db      181 GTGACCCCTCTGTGAGGATAGTAAAGTCAACCTCTCCCTGTAAGAACAGATCATT 240
OY      241 TCCCTTGAGGAATGATCCACCTGAAATATATGATGATATACAAAGTATCATATTC 300
Db      241 TCCCTTGAGGAATGATCCACCTGAAATATATGATGATATACAAAGTATCATATTC 300
OY      301 TTTCAGAAAGCTGTCCAGACACACAAGAGAGAGTTCGATCTTCACTGATAGAGA 360
Db      301 TTTCAGAAAGCTGTCCAGACACACAAGAGAGTTCGATCTTCACTGATAGAGA 360
OY      361 CACTTCTGCTTGCCAAAGAGATGATGCTTCAAACTCATCTGAAAAAAGAGAT 420
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OY      421 GAAATGGGGATTAATCTGTAATGTCACCTCTCACTACTACTACATCAAGT 471
Db      421 GAAATGGGGATTAATCTGTAATGTCACCTCTCACTACTACTACATCAAGT 471
OY      8
ID      E12010 standard; RNA; ROD; 471 BP.
AC      E12010;
SV      E12010.1
DT      07-OCT-1997 (Rel. 52, Created)
DT      07-OCT-1997 (Rel. 52, Last updated, Version 1)
DE      cDNA encoding mouse polypeptide which introduce interferon-gamma product in
DE      immunocompetent cell.
XX      JP 1996231598-A/2.
XX      Mus musculus (house mouse)
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
XX      [1]
XX      RP 1-471
XX      RA Kunikata T., Taniguchi M., Kono K., Kurimoto M.;
XX      RT "MONOCLONAL ANTIBODY";
XX      RL Patent number JP 1996231598-A/2, 10-SEP-1996.
XX      HAYASHIBARA BIOCHEM LAB INC.
XX      OS Mus musculus (mouse)
XX      CC PN JP 1996231598-A/2
XX      CC PD 10-SEP-1996
XX      CC PF 23-FEB-1995 JP 1995058240
XX      CC PI KUNIKATA TOSHIO, TANIGUCHI MUTSUOKO, KONO KEIZO,
XX      CC PC C07K16/24, C07K16, C07K1/18, C07K1/22, C07K1/26, C07K1/30,
XX      CC PC C07K1/34, C12N5/10,
XX      CC PC C12N15/02, C12P21/08, G01N33/53, G01N33/57//A61K38/21, A61K39/395,
XX      CC PC C12P21/08,
XX      CC PC C12R1(91);
XX      CC CC Strandedness: Double;
XX      CC CC Topology: Linear;
XX      CC CC Hypothesis: No;
XX      CC CC anti-sense: No;
XX      CC FH Key
XX      CC FH source
XX      CC FH 1. 471
XX      CC FH /organism="Mus musculus"
XX      CC FH /tissue_type="liver"
XX      FH Key
FH      Location/Qualifiers

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FT      source
FT      1. 471
FT      /db_xref="taxon:10090"
FT      /organism="Mus musculus"
SQ      Sequence 471 BP; 162 A; 91 C; 92 G; 125 T; 1 other;

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Query Match      99.9%; Score 470.6; DB 22; Length 471;
Best Local Similarity 100.0%; Pred. No. 1.3e-103;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 AACTTGGCCCACTTCACTGATACACCGCACTAATACGAATATTAATGACCAAGTCTC 60
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Db      301 TTTCAGAAAGCTGTCCAGACACACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
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OY      421 GAAATGGGGATTAATCTGTAATGTCACCTCTCACTACTACTACATCAAGT 471
Db      421 GAAATGGGGATTAATCTGTAATGTCACCTCTCACTACTACTACATCAAGT 471

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RESULT 9
MUSIGIPP 866 bp mRNA ROD 10-FEB-1999
LOCUS Mouse mRNA for IGF precursor polypeptide, complete cds.
DEFINITION D49949.1 GI:1064822
VERSION IGF precursor polypeptide.
KEYWORDS Mus musculus liver cDNA to mRNA, clone pMUGF7B-5.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
REFERENCE 1 (bases 1 to 866)
AUTHORS Okamura, H.
TITLE Direct Submission
JOURNAL Submitted (29-MAR-1995) to the DDBJ/EMBL/GenBank databases. Haruki-
Mukogawa 1-1, Nishinomiya, Hyogo 663, Japan (Tel:0798-45-6111)
2 (bases 1 to 866)
AUTHORS Okamura, H., Tsutsumi, H., Komatsu, T., Yutsudo, M., Hakura, A.,
Tanimoto, T., Torisoe, K., Okura, T., Nukada, Y., Hattori, K., Akita, K.,
Namba, M., Tanabe, F., Konishi, K., Fukuda, S. and Kurimoto, M.
TITLE Cloning of a new cytokine that induces IFN-gamma production by T
cells
JOURNAL Nature 378 (6552), 88-91 (1995)
MEDLINE 9606109
FEATURES
source Location/Qualifiers
1. 866
/organism="Mus musculus"
/db_xref="taxon:10090"

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CDS
/tissue_type="liver"
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165..743
/product="IGIF precursor polypeptide"
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/db_xref="GI:1064823"
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SKMSYLSCKNKIISFEEDPPEPIDIOSDLFFOKRVPGHNMKEFESSLYEGHFLAC
OKEDAFKILKKDENGDKSVFTLTNLHOS"
866

polyA_site 262 a 187 c 187 g 230 t
BASE COUNT
ORIGIN

Query Match 99.9%; Score 470.6; DB 12; Length 866;
Best Local Similarity 99.8%; Pred. No. 1.3e-103;
Matches 470; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACTTTGGCCGACTTACTGTACACCGCAGTATACGGAATTAATGACCAAGTTCTC 60
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DB 270 AACTTTGGCCGACTTACTGTACACCGCAGTATACGGAATTAATGACCAAGTTCTC 329
OY 61 TTGCTGACAAAAGACAGCCTGTGTCGAGATATGACTGATTTGATCAAGTGCAGT 120
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DB 330 TTGCTGACAAAAGACAGCCTGTGTCGAGATATGACTGATTTGATCAAGTGCAGT 389
OY 121 GAACCCAGACAGCAGTATATATACATGTACAAAGACAGTAAAGAGAGTGGCT 180
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DB 390 GAACCCAGACAGCAGTATATATACATGTACAAAGACAGTAAAGAGAGTGGCT 449
OY 181 GTGACCCCTCTGTGTGAAGATAGTAAATGTCACCTCTCCTGTGAAGACAGATCAT 240
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DB 450 GTGACCCCTCTGTGTGAAGATAGTAAATGTCACCTCTCCTGTGAAGACAGATCAT 509
OY 241 TCCCTTGAGAGAAATGATCCACTGAAATATATGATGATATACAAAGTATCATATT 300
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DB 510 TCCCTTGAGAGAAATGATCCACTGAAATATATGATGATATACAAAGTATCATATT 569
OY 301 TTTCAGAAACGTTTCCAGACACAAACAGATGAGATTGGAATCTTCACTGTATGAAGA 360
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DB 570 TTTCAGAAACGTTTCCAGACACAAACAGATGAGATTGGAATCTTCACTGTATGAAGA 629
OY 361 CACTTCTTCTGCTTCCAAAAGAGATGATGCTTTCAACTCATTTGAAAAAAGAGAT 420
|||||
DB 630 CACTTCTTCTGCTTCCAAAAGAGATGATGCTTTCAACTCATTTGAAAAAAGAGAT 689
OY 421 GAAATATGGGATTAATCTGTATGTTCACTCTCACTACTTACATCAAACT 471
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DB 690 GAAATATGGGATTAATCTGTATGTTCACTCTCACTACTTACATCAAACT 740

RESULT 10
MM066244 572 bp mrna ROD 18-MAR-1997
LOCUS MM066244
DEFINITION Mus musculus interferon-gamma inducing factor mRNA, partial cds.
VERSION U066244.1 GI:1561735
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 572)
AUTHORS Rothe,H., Jenkins,N.A., Copeland,N.G. and Kolb,H.
TITLE Active stage of autoimmune diabetes is associated with the expression of a novel cytokine, IGIF, which is located near Idd2
JOURNAL J. Clin. Invest. 99 (3), 468-474 (1997).
MEDLINE 97174346
REFERENCE 2 (bases 1 to 572)
AUTHORS Rothe,H., Copeland,N.G. and Kolb,H.

TITLE Direct Submission
JOURNAL Submitted (06-AUG-1996) Diabetes Research Institute, Aufm
Hennekamp 65, Duesseldorf 40225, Germany
FEATURES
source
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/strain="non obese diabetic (NOD)"
/db_xref="taxon:10090"
/chromosome="9"
/tissue_type="pancreas"
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/note="IGIF"
/codon_start=1
/product="interferon gamma inducing factor"
/protein_id="AAB49753.1"
/db_xref="GI:1561736"
/translation="MAAISEDSCVNFKEKMFIDNTLYFIPEENGDESDFRLHCTT
AVIRNIINOVLVDKROPVEEDMTIDOSASEPOTRLIYMKDSEVRGLAVTSLVKD
SKMSYLSCKNKIISFEEDPPEPIDIOSDLFFOKRVPGHNMKEFESSLYEGHFLAC
OKEDAFKILKKDENGDKSVISLTNLHOS"

BASE COUNT 196 a 111 c 113 g 152 t
ORIGIN

Query Match 96.0%; Score 452; DB 12; Length 572;
Best Local Similarity 98.9%; Pred. No. 3.9e-99;
Matches 465; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

OY 1 AACTTTGGCCGACTTACTGTACACCGCAGTATACGGAATTAATGACCAAGTTCTC 60
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DB 106 AACTTTGGCCGACTTACTGTACACCGCAGTATACGGAATTAATGACCAAGTTCTC 165
OY 61 TTGCTGACAAAAGACAGCCTGTGTCGAGATATGACTGATTTGATCAAGTGCAGT 120
|||||
DB 166 TTGCTGACAAAAGACAGCCTGTGTCGAGATATGACTGATTTGATCAAGTGCAGT 225
OY 121 GAACCCAGACAGCAGTATATATACATGTACAAAGACAGTAAAGAGAGTGGCT 180
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DB 226 GAACCCAGACAGCAGTATATATACATGTACAAAGACAGTAAAGAGAGTGGCT 285
OY 181 GTGACCCCTCTGTGTGAAGATAGTAAATGTCACCTCTCCTGTGAAGACAGATCAT 240
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DB 286 GTGACCCCTCTGTGTGAAGATAGTAAATGTCACCTCTCCTGTGAAGACAGATCAT 345
OY 241 TCCCTTGAGAGAAATGATCCACTGAAATATATGATGATATACAAAGTATCATATT 300
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DB 346 TCCCTTGAGAGAAATGATCCACTGAAATATATGATGATATACAAAGTATCATATT 405
OY 301 TTTCAGAAACGTTTCCAGACACAAACAGATGAGATTGGAATCTTCACTGTATGAAGA 360
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DB 406 TTTCAGAAACGTTTCCAGACACAAACAGATGAGATTGGAATCTTCACTGTATGAAGA 465
OY 361 CACTTCTTCTGCTTCCAAAAGAGATGATGCTTTCAACTCATTTGAAAAAAGAGAT 420
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DB 466 CACTTCTTCTGCTTCCAAAAGAGATGATGCTTTCAACTCATTTGAAAAAAGAGAT 525
OY 421 GAAATATGGGATTAATCTGTATGTTCACTCTCACTACTTACATCAAACT 470
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DB 526 GAAATATGGGATTAATCTGTATGTTCACTCTCACTACTTACATCAAACT 572

RESULT 11
RNU07776 722 bp mrna ROD 31-JAN-1997
LOCUS RNU07776
DEFINITION Rattus norvegicus interferon-gamma inducing factor precursor (IGIF)
ACCESSION U07776
VERSION U07776.1 GI:1809128
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 722)
 AUTHORS Conti,B., Jahng,J.W., Tinti,C., Son,J.H. and Joh,T.H.
 TITLE Induction of interferon-gamma inducing factor in the adrenal cortex
 JOURNAL J. Biol. Chem. 272 (4), 2035-2037 (1997)
 MEDLINE 97152963
 REFERENCE 2 (bases 1 to 722)
 AUTHORS Conti,B., Jahng,J.W., Tinti,C., Son,J.H. and Joh,T.H.
 TITLE Direct Submission
 JOURNAL Submitted (08-NOV-1996) Molecular Neurobiology, Cornell University
 Medical College at Burke Research Institute, 785 Mamaroneck Ave,
 White Plains, NY 10605, USA

FEATURES

source

1..722
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"

gene

1..585
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 /gene="IGIF"

CDS

1..585
 /gene="IGIF"
 /codon_start=1
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 /protein_id="AAC53009.1"
 /db_xref="GI:1809129"

BASE COUNT

252 a 138 c 140 g 192 t

ORIGIN

 TAVTASINDOVLFDKRNPPVFEEDPDIDRANESOTRLITMYKDSVRLAVLSY
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Query Match

Best Local Similarity 85.1%; Score 400.6; DB 12; Length 722;
 Matches 434; Conservative 1; Mismatches 35; Indels 3; Gaps 1;

2 ACTTTGGCCGACTTCACTGTACACCGCAGTATACGAAATTAATGACCAAGTTCTCT 61
 110 ACTTTGGCAGACTTCACTGTACACCGCAGTATACGAAATTAATGACCAAGTTCTCT 169
 62 TCGTTGACAAAGA--CAGCTGTGTTGAGAGATATGACTGATATTGATCAAAAGTGCCA 118
 170 TCGTTGACAAAGAACCAGCTGTGTTGAGAGATATGACTGATATTGATCAAAAGTGCCA 229
 119 GNGAACCCGACGACGATGATATATACATGATACAAAGAGAGAGAGAGAGAGAGAGAG 178
 230 ACGAAATCCGACGACGATGATATATATATATATATATATATATATATATATATATAT 289
 179 CTGTGACCTCTCTGTGAGAGATAGTAAATATGATACCTCTCTGTGAGAGATAGTAA 238
 290 CTGTGACCTCTCTGTGAGAGATAGTAAATATGATACCTCTCTGTGAGAGATAGTAA 349
 239 TTTCTTTGAGAGAAATGATGACCTGAAATATGATGATATACAAAGTATCTCATAT 298
 350 TTTCTTTGAGAGAAATGATGACCTGAAATATGATGATATACAAAGTATCTCATAT 409
 299 TCTTTCAAGAAAGTGTTCCAGACACACAGATGAGTTGATGATCTCTGATGAG 358
 410 TCTTTCAAGAAAGTGTTCCAGACACACAGATGAGTTGATGATCTCTGATGAG 469
 359 GACACTTTCTCTGTTCCAGACACACAGATGAGTTGATGATCTCTGATGAG 418
 470 GACACTTTCTCTGTTCCAGACACACAGATGAGTTGATGATCTCTGATGAG 529
 419 ATGAAATGAGGATATATCTGATGATGATGATGATGATGATGATGATGATGATGAT 471
 530 ATGAAATGAGGATATATCTGATGATGATGATGATGATGATGATGATGATGATGAT 582

RESULT 127

RNAJB13

LOCUS

RNAJB13

628 bp mRNA

11-AUG-1998

DEFINITION

Rattus norvegicus mRNA for precursor interleukin 18 (IL-18), complete cds.

ACCESSION

AJ222813

VERSION

AJ222813.1 GI:3413501

KEYWORDS

IL-18 gene; interleukin.

SOURCE

Norway rat.

ORANISM

Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE

1 (bases 1 to 628)
 Culhane,A.C., Hall,M.D., Rothwell,N.J. and Lubeshi,G.N.
 Cloning of rat brain interleukin-18 cDNA
 Mol. Psych. 3, 362-366 (1998)

AUTHORS

Culhane,A.C.

TITLE

Direct Submission
 Submitted (08-DEC-1997) Culhane A.C., University of Manchester,
 School of Biological Sciences, 1.124 Stopford Building, Manchester,
 Lancs, M13 9PT, UK

FEATURES

Location/Qualifiers
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 /strain="Sprague dawley"
 /db_xref="taxon:10116"

gene

/clone="rat IL-18"
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CDS

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 factor; interleukin-1 gamma"
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 /protein_id="CAA11001.1"
 /db_xref="GI:3413502"

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 ACQKEDDAFKVLKRDENGDKSVMTLTNLHOS"
 109..582
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 and cytotoxic T cells."
 /product="Precursor IL-18 is cleaved at Asp-His by
 caspase-1; mature IL-18"
 109..582

BASE COUNT

216 a 120 c 126 g 166 t

ORIGIN

Query Match

Best Local Similarity 84.0%; Score 395.8; DB 12; Length 628;
 Matches 431; Conservative 1; Mismatches 38; Indels 3; Gaps 1;

2 ACTTTGGCCGACTTCACTGTACACCGCAGTATACGAAATTAATGACCAAGTTCTCT 61
 110 ACTTTGGCAGACTTCACTGTACACCGCAGTATACGAAATTAATGACCAAGTTCTCT 169
 62 TCGTTGACAAAGA--CAGCTGTGTTGAGAGATATGACTGATATTGATCAAAAGTGCCA 118
 170 TCGTTGACAAAGAACCAGCTGTGTTGAGAGATATGACTGATATTGATCAAAAGTGCCA 229
 119 GNGAACCCGACGACGATGATATATACATGATACAAAGAGAGAGAGAGAGAGAGAGAG 178
 230 ACGAAATCCGACGACGATGATATATATATATATATATATATATATATATATATATAT 289
 179 CTGTGACCTCTCTGTGAGAGATAGTAAATATGATACCTCTCTGTGAGAGATAGTAA 238
 290 CTGTGACCTCTCTGTGAGAGATAGTAAATATGATACCTCTCTGTGAGAGATAGTAA 349

Qy 1 AACTTTGGCCGACCTTCACTGTACAACCGCAGTAATACGGAAATAAANGACCMACTTC 60
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KDGMRSTLSCCKNKIISFEKRVPGHNKMEFESSLYEGHFLACQEDDAFKLVLKRDDE
GDKSVMTLITNLHOS"

BASE COUNT 229 a 130 c 132 g 174 t
ORIGIN

Query Match 59.4%; Score 279.8; DB 12; Length 665;
Best Local Similarity 80.1%; Pred. No. 1.3e-57;
Matches 379; Conservative 1; Mismatches 33; Indels 60; Gaps 2;

OY 2 ACTTTGGCCGACCTGCTAGTACACCCGACATATATAGCAATATATATAGCAAGTCTCT 61
DB 110 ACTTTGGCCGACCTGCTAGTACACCCGACATATATAGCAATATATATAGCAAGTCTCT 169
OY 62 TCGTTGACAAAAGA--CAGCTGTGTTCGAGATATAGTATATATATATATATATATATAT 118
DB 170 TCGTTGACAAAAGAAGACCCGCTGTGTTCGAGATATAGTATATATATATATATATATAT 229
OY 119 GTGACCCGACGACGACGAT 178
DB 230 ACAGATCCGACGACGAT 289
OY 179 CTGTGACCTCTCTGTGAGATAGTAAATGTACCCCTCTCTGTGAGATAGTAAATAGTAA 238
DB 290 CTGTGACCTCTCTGTGAGATAGTAAATGTACCCCTCTCTGTGAGATAGTAAATAGTAA 349
OY 239 TTTCCTTTGAGAAATGATCCACCTGAAATATATGATGATATATATATATATATATATAT 298
DB 350 TTTCCTTTG----- 358
OY 299 TCTTTGAGAACTGTTCAGACACACAGATGAGTTGATCTTCTGATGATGAG 358
DB 359 -----AGAAACGTGTGCGAGACACACAGAAATGAGTTGATCTTCTGATGATGAG 412
OY 359 GACACTTTTGTGCTGCAAAAGAGATGATGCTTCAACGATCTTCAAGTCAAGTCAAG 418
DB 413 GACACTTTTGTGCTGCAAAAGAGATGATGCTTCAACGATCTTCAAGTCAAGTCAAG 472
OY 419 ATGAAATGAGGATTAATCTGTAATGTTCACTCTCACTTCACTTCACTTCACTTCACTTCA 471
DB 473 ATGAAATGAGGATTAATCTGTAATGTTCACTCTCACTTCACTTCACTTCACTTCACTTCA 525

RESULT 15

LOCUS ASIGIF 471 bp DNA SYN 08-NOV-1996
DEFINITION Artificial sequence DNA for cytokine interferon-gamma inducing factor (IGIF).
ACCESSION Y09278
VERSION Y09278.1 GI:1666283
KEYWORDS cytokine; interferon-gamma inducing factor (IGIF).
SOURCE synthetic construct.
ORGANISM Schluesener, H.J.
REFERENCE 1 (bases 1 to 471)
JOURNAL Unpublished
AUTHORS Schluesener, H.J.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-1996) H.J. Schluesener, Inst. f. Hirnforschung, Calwer Str. 3, D-77076 Tuebingen, FRG
FEATURES
Location/Qualifiers
1..471
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BASE COUNT 148 a 100 c 130 g 93 t
ORIGIN

Query Match 59.3%; Score 279.2; DB 13; Length 471;
Best Local Similarity 74.5%; Pred. No. 1.8e-57;
Matches 350; Conservative 1; Mismatches 119; Indels 0; Gaps 0;

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DB 1 AACTTTGGCCGACCTGCTAGTACACCCGACATATATAGCAATATATATAGCAAGTCTCT 60
OY 61 TCGTTGACAAAAGAAGACCCGCTGTGTTCGAGATATAGTATATATATATATATATATATAT 120
DB 61 TCGTTGACAAAAGAAGACCCGCTGTGTTCGAGATATAGTATATATATATATATATATATAT 120
OY 121 GAACCCGACGACGACGAT 180
DB 121 GAACCCGACGACGAT 180
OY 181 GTGACCTCTCTGTGAGATAGTAAATGTACCCCTCTCTGTGAGATAGTAAATAGTAA 240
DB 181 GTGACCTCTCTGTGAGATAGTAAATGTACCCCTCTCTGTGAGATAGTAAATAGTAA 240
OY 241 TCTTTGAGAAATGATCCACCTGAAATATATGATGATATATATATATATATATATATAT 300
DB 241 AGCTTGAAGAAATGAGACCCCGCGAAACATCATGATATATATATATATATATATATAT 300
OY 301 TTTCGAGAACTGTTCAGACACACAGATGAGTTGATCTTCTGATGATGAG 360
DB 301 TTTCGAGAACTGTTCAGACACACAGATGAGTTGATCTTCTGATGATGAG 360
OY 361 CACTTTCTTGTCTGCCAAAAGAGATGATCTTCAACGATCTTCAAGTCAAGTCAAG 420
DB 361 CACTTTCTTGTCTGCCAAAAGAGATGATCTTCAACGATCTTCAAGTCAAGTCAAG 420
OY 421 GAAATGAGGATTAATCTGTAATGTTCACTCTCACTTCACTTCACTTCACTTCACTTCA 470
DB 421 GAAATGAGGATTAATCTGTAATGTTCACTCTCACTTCACTTCACTTCACTTCACTTCA 470

Search completed: November 21, 2000, 21:29:12
Job time: 15174 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 21, 2000, 21:13:24 : Search time 39.29 Seconds
(without alignments)
136.636 Million cell updates/sec

Title: US-09-050-249-2

Perfect score: 808
Sequence: 1 NFRSLHCTATVIRINQVVL.....KKDENGKSVMTLTINLHOS 157

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

A.Geneseq.36:*

- 1: /cgn2_2/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /cgn2_2/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /cgn2_2/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /cgn2_2/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /cgn2_2/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /cgn2_2/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /cgn2_2/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /cgn2_2/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /cgn2_2/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /cgn2_2/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /cgn2_2/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /cgn2_2/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /cgn2_2/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /cgn2_2/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /cgn2_2/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /cgn2_2/gcgdata/geneseq/geneseq/AA1995.DAT:*
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- 18: /cgn2_2/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /cgn2_2/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /cgn2_2/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /cgn2_2/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	806	99.8	157	R99559	Mouse mature inter
2	806	99.8	157	R92506	Interferon gamma p
3	806	99.8	157	W15704	Mouse interferon-g
4	806	99.8	157	W24262	Murine protein for
5	806	99.8	157	W77078	Mouse interleukin
6	806	99.8	157	W77159	Murine interleukin
7	806	99.8	157	W63811	Mouse IL-18 protei
8	806	99.8	157	Y39800	Interleukin-18 rec
9	806	99.8	157	Y44598	Mouse monomeric in
10	806	99.8	157	Y53905	Amino acid sequenc
11	806	99.8	157	Y57571	Murine interleukin
12	806	99.8	180	W48960	Wild-type mouse in

13	797	98.6	157	19	W77090	Mouse interleukin
14	797	98.6	157	19	W48968	Mutant mouse inter
15	796	98.5	157	19	W77091	Mouse interleukin
16	796	98.5	157	19	W48969	Mutant mouse inter
17	736.5	91.2	154	19	W53282	Amino acid sequenc
18	6251	77.4	195	19	Y58241	Amino acid sequenc
19	538	66.6	193	21	W77084	Equine interleukin
20	524	64.9	157	19	W77084	Human interleukin
21	524	64.9	157	19	W48962	Mutant human inter
22	521	64.5	157	19	W77083	Human interleukin
23	521	64.5	157	19	W48961	Mutant human inter
24	518	64.1	157	19	W77077	Human interleukin
25	518	64.1	157	21	Y57570	Human interleukin
26	518	64.1	158	21	Y85167	Human interleukin
27	518	64.1	180	19	W48959	Wild-type human in
28	518	64.1	193	18	W22047	Interferon gamma i
29	518	64.1	193	19	W48962	Amino acid sequenc
30	515	63.7	157	19	W77080	Human interleukin
31	515	63.7	157	19	W77088	Human interleukin
32	515	63.7	157	19	W48966	Mutant human inter
33	515	63.7	193	19	W77082	Interleukin 18 act
34	514	63.6	157	19	W77086	Human interleukin
35	514	63.6	157	19	W48964	Mutant human inter
36	513	63.5	157	17	R99558	Human interleukin-g
37	513	63.5	157	17	R99558	Human mature inter
38	513	63.5	157	18	W15701	Interferon-gamma i
39	513	63.5	157	18	W24258	Human protein for
40	513	63.5	157	19	W77158	Human interleukin
41	513	63.5	157	19	W63810	Human IL-18 protei
42	513	63.5	157	19	W37741	IFN-gamma inducing
43	513	63.5	157	19	W52176	Interleukin-gamma i
44	513	63.5	157	20	Y39799	Interleukin-18 rec
45	513	63.5	157	21	Y44597	Human interleukin-

ALIGNMENTS

RESULT	1
R99559	
ID	R99559 standard; Protein: 157 AA.
XX	
AC	R99559;
XX	
DT	29-SEP-1996 (first entry)
XX	
DE	Mouse mature interferon-gamma inducer protein.
XX	
KW	Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;
KW	antitumor; antibacterial; immunoregulator; adoptive immunotherapy;
KW	therapy; cancer.
XX	
OS	Mus sp.
XX	
FT	Key
FT	Misc-difference 70
FT	/label=1le, Thr
XX	
PN	EP712931-A2
XX	
PD	22-MAY-1996.
XX	
XX	95EP-0308055.
PF	10-NOV-1995.
XX	
PR	29-SEP-1995. 95JP-0274988.
XX	
PR	15-NOV-1994. 94JP-0304203.
XX	
PR	23-FEB-1995. 95JP-00588240.
XX	
PR	10-MAR-1995. 95JP-0078357.
XX	
PR	18-SEP-1995. 95JP-0262062.
XX	
PA	(HAYB) HAYASHIBARA SEIBOTSU KAGANKU.
XX	
PI	Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;

PI Taniguchi M, Tanimoto T, Torigoe K, Ushio S;
 XX
 DR WPI: 1996-252837/26.
 DR N-PSDB: T92403.
 XX
 PT DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
 PT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders
 XX
 PS Example A-3-2; Page 36-37; 48pp; English.
 XX
 CC A novel mouse protein (R99559) induces interferon-gamma (IFN-gamma)
 CC prodn. by immunocompetent cells. Its sequence was deduced from
 CC that of a cDNA clone (T32403) isolated from a mouse liver library.
 CC Recombinant IFN-gamma inducer protein can be produced in high yields
 CC using host cells, esp. Escherichia coli, transformed with a vector
 CC carrying the cDNA.
 CC
 SO Sequence 157 AA;
 XX
 Query Match 99.8%; Score 806; DB 17; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NEGRHCTAVIRNINDQVLFVDRKQPVFEDMTDIDQASAPQRLIIMYKDEVRGIA 60
 DB 1 ngrhctavirndqylfvdkrqpvedmtidqasapqrlilimykdevrigia 60
 OY 61 VTLVSKDSKXSTLSCKNKLIISFEEMDPENIDIOSDLIFQKRVPGHNKMEFESSLYEG 120
 DB 61 vtlsvkdsksxstlscknkliisfeemdpenniiddiqsdliiffqkrvpgnhkmeffesslyeg 120
 OY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHQS 157
 DB 121 hflacqkedafkllilkkkdehgdksvmftltlnhqs 157
 RESULT 2
 R92506 standard; Protein; 157 AA.
 AC R92506;
 XX
 DT 02-SEP-1996 (first entry)
 XX
 DE Interferon gamma production inducer protein.
 XX
 KW Interferon gamma; inducer; IFNgamma; immunocompetent cell; antiviral;
 KW antitumour; antiseptic; immunoregulatory; platelet-increasing agent;
 KW therapy; prevention; condyloma acuminatum; renal cancer; brain cancer;
 KW granuloma; mycosis fungoides; rheumatism; allergy; cytotoxicity; AIDS;
 KW killer T-cell; interleukin-2; IL-2; tumour necrosis factor; TNF;
 KW adoptive immunotherapy; monoclonal antibody.
 KW
 XX
 OS Mus musculus.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 70 /label= Met, Thr
 FT
 XX
 XX EP692536-A2.
 XX
 PD 17-JAN-1996.
 XX
 PF 13-JUL-1995; 95EP-0304906.
 XX
 PR 10-FEB-1995; 95JP-0045057.
 PR 14-JUL-1994; 94JP-0184162.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Kohno K, Kunikata T, Kurimoto M, Okamura H, Taniguchi M;

PI Tanimoto T, Torigoe K;
 XX
 DR WPI: 1996-070177/08.
 DR N-PSDB: T92506.
 XX
 PT Protein that induces gamma interferon prodn. in immuno:competent
 PT cells - used e.g. as antiviral or antitumour agent, also induces
 PT cytotoxicity of killer cells
 XX
 PS Claim 2; Page 22; 30pp; English.
 XX
 CC This sequence represents the interferon gamma (IFNgamma) inducer protein
 CC of the invention. This protein induces IFNgamma production in
 CC immunocompetent cells. The protein is useful as an antiviral,
 CC antitumour, antiseptic, immunoregulatory and platelet-increasing agent.
 CC It can be used for treating or preventing AIDS, condyloma acuminatum,
 CC renal or brain cancer, granuloma, mycosis fungoides, rheumatism and
 CC allergy. The protein can also be used to induce IFNgamma production in
 CC cultured cells. The IFNgamma inducer strongly induces cytotoxicity of
 CC killer T-cells and when used with interleukin-2 (IL-2) and tumour
 CC necrosis factor (TNF), may improve the effect (or reduce side effects) of
 CC adoptive immunotherapy in tumours. The DNA encoding this sequence can
 CC be used to produce the protein, which can then be purified (or assayed)
 CC using monoclonal antibodies.
 CC
 SO Sequence 157 AA;
 XX
 Query Match 99.8%; Score 806; DB 17; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NEGRHCTAVIRNINDQVLFVDRKQPVFEDMTDIDQASAPQRLIIMYKDEVRGIA 60
 DB 1 ngrhctavirndqylfvdkrqpvedmtidqasapqrlilimykdevrigia 60
 OY 61 VTLVSKDSKXSTLSCKNKLIISFEEMDPENIDIOSDLIFQKRVPGHNKMEFESSLYEG 120
 DB 61 vtlsvkdsksxstlscknkliisfeemdpenniiddiqsdliiffqkrvpgnhkmeffesslyeg 120
 OY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHQS 157
 DB 121 hflacqkedafkllilkkkdehgdksvmftltlnhqs 157
 RESULT 3
 W15704 standard; Peptide; 157 AA.
 ID W15704;
 AC W15704;
 XX
 DT 26-JAN-1998 (first entry)
 XX
 DE Mouse interferon-gamma inducer protein.
 XX
 KW Interferon-gamma, IFN-gamma; antiviral; antitumour; radiotherapy;
 KW immunoregulatory; antitumour agent; chemotherapy; leukaemia;
 KW thrombocytopaenia; immunocompetent cell; asthma; hayfever;
 KW rheumatism; interleukin; killer cell.
 KW
 XX
 OS Mus musculus.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 70 /label= Met, Thr
 FT
 XX
 XX EP767178-A1.
 XX
 PD 09-APR-1997.
 XX
 PF 26-SEP-1996; 96EP-0306997.
 XX
 PR 20-SEP-1996; 96JP-0269105.

PR 26-SEP-1995: 95JP-0270725.
 PR 29-FEB-1996: 96JP-0067434.
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T;
 DR WPI: 1997-205381/19.
 DR N-PSDB: T60536.
 XX
 PT Human protein that induces interferon-gamma prodn. in
 PT immuno:competent cells - useful for adoptive immuno:therapy of
 PT tumours and as antimicrobial agent etc.
 PS
 PS Disclosure: Page 22: 26pp; English.
 XX
 CC The present sequence represents a novel protein from mouse liver cells,
 CC which induces interferon-gamma (IFN gamma) production in immunocompetent
 CC cells. This protein enhances cytotoxicity of killer cells and induces
 CC their formation. It is used as an antitumor agent for antitumor
 CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,
 CC and in the treatment of atopic or immune system diseases, e.g. asthma,
 CC hayfever or rheumatism. When formulated with interleukin-3, it is also
 CC used to treat leukopenia and thrombocytopenia associated with
 CC radiotherapy or chemotherapy of leukaemia and other cancers. When used
 CC in antitumor immunotherapy, this novel protein significantly improves
 CC the immunotherapeutic effect of interleukin-2 (IL-2), compared with use
 CC of IL-2 alone, either when administered to the patient (before
 CC administration of IL-2) or by addition to the medium in which cells
 CC (intended for return to the patient) are being grown.
 XX
 SQ Sequence 157 AA;

Query Match 99.8%: Score 806; DB 18; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NEGRHCTTAVIRININDVLFVDRKROPVEEDMTDIDOSASEPOTRLIITYMKDSEVRGLA 60
 Db 1 ngrhcttavrinnndvylfvdkrqpvefemtdidgsasepqrllllymkdsevrsla 60
 QY 61 VLSVYKDSKXSTLSCNKKIISFEEMDPENIDDIOSDLIFQKRVPGHKKMEFESSLYEG 120
 Db 61 vlsvykdsksxlscnkkisfeemdpenniddisdliffqkrvpgnhkmeffesslyeg 120
 QY 121 HFLACOKEDDAFKLILKKKDKSGKSVFTLTNLHOS 157
 Db 121 hflacokeddafklllkkkdksgksvmftltlnhgs 157

RESULT 4
 ID W24262 standard; Protein: 157 AA.
 AC W24262:
 XX
 DT 15-OCT-1997 (first entry)
 XX
 DE Murine protein for induction of interferon-gamma.
 XX
 KW Interferon-gamma; immunocompetent cell; malignant tumour;
 KW viral disease; bacterial infection; immune disease.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 70 /note= "Encoded by AYT"
 XX
 PN JP09157180-A.
 XX
 PD 17-JUN-1997.

XX
 PF 24-JAN-1996: 96JP-0028722.
 XX
 PR 04-OCT-1995: 95JP-0279906.
 PR 10-MAR-1995: 95JP-0078357.
 PR 29-SEP-1995: 95JP-0274968.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 DR WPI: 1997-369391/34.
 DR N-PSDB: T80210.
 XX
 PT A drug containing a polypeptide which induces interferon-gamma -
 PT useful for treating e.g. malignant tumours, viral, bacterial or
 PT immune diseases
 PS
 PS Disclosure: Page 10-11: 12pp; Japanese.
 XX
 CC This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 XX
 SQ Sequence 157 AA;

Query Match 99.8%: Score 806; DB 18; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NEGRHCTTAVIRININDVLFVDRKROPVEEDMTDIDOSASEPOTRLIITYMKDSEVRGLA 60
 Db 1 ngrhcttavrinnndvylfvdkrqpvefemtdidgsasepqrllllymkdsevrsla 60
 QY 61 VLSVYKDSKXSTLSCNKKIISFEEMDPENIDDIOSDLIFQKRVPGHKKMEFESSLYEG 120
 Db 61 vlsvykdsksxlscnkkisfeemdpenniddisdliffqkrvpgnhkmeffesslyeg 120
 QY 121 HFLACOKEDDAFKLILKKKDKSGKSVFTLTNLHOS 157
 Db 121 hflacokeddafklllkkkdksgksvmftltlnhgs 157

RESULT 5
 ID W77078 standard; Protein: 157 AA.
 AC W77078:
 XX
 DT 14-DEC-1998 (first entry)
 XX
 DE Mouse interleukin 18 protein.
 XX
 KW Mouse; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 KW osteoclastoma; Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 KW chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.
 XX
 OS Mus sp.
 XX
 PN EP861663-A2.
 PD 02-SEP-1998.
 XX
 DT 24-FEB-1998: 98EP-0301352.
 PR 25-FEB-1997: 97JP-0055468.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
 XX
 DR WPI: 1998-448964/39.

DR N-PSDB; V48227.
 XX Use of interleukin-18 to inhibit osteoclast formation - in treatment
 PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 PT osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
 PT primary hyperthyroidism and osteoporosis
 XX Claim 6; Page 19; 56pp; English.
 CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 XX
 SQ Sequence 157 AA:
 Query Match 99.8%; Score 806; DB 19; Length 157;
 Best Local Similarity 99.4%; Pred. No. 6.2e-79;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NFGRLHCTTAVIRNINDQVLFVDRKQVPEEDMDIDQASASEPQRLIITYMKDSEVRGLA 60
 ID 1 nfgrlhcttavrindqvlfvdkrqpvedmdidqasasepqrllitymkdsevrghla 60
 QY 61 VTLTVSKSKXSTLSCKNKIISFEEMDPENIDIDQSLIFPQKRVPGHNKMEFESSLYEG 120
 DB 61 vtltsvkkskstlscnklisfeemdpennididqsliffqkrvpgnkmefesslyeg 120
 QY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLLNLHQS 157
 DB 121 hflacqkedafrklilkkkdengdksvmtllnlhqs 157
 RESULT 6
 W77159
 ID W77159 standard; Protein; 157 AA.
 AC W77159;
 XX
 DT 26-NOV-1998 (first entry)
 XX
 DE Murine interleukin-18 protein (IL-18).
 XX
 KM Murine; interleukin-18 receptor; IL-18; cytokine; signal transduction;
 KM immune system; treatment; autoimmune; allergic disease;
 KM immunosuppressant.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 70 /note="Met or Thr"
 FT
 XX
 PN EP864585-A1.
 PD 16-SEP-1998.
 XX
 PF 23-DEC-1997; 97EP-0310517.
 XX
 PR 09-OCT-1997; 97JP-0291837.
 PR 12-MAR-1997; 97JP-0074697.
 PR 28-JUL-1997; 97JP-0215488.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Kurimoto M, Okura T, Torigoe K;
 XX
 DR WPI; 1998-469188/41.
 XX
 PT Interleukin-18 receptor polypeptide(s) - and corresponding DNA,

PT which peptide compounds are useful for treating auto-immune or
 PT allergic diseases
 XX
 XX Disclosure; Page 42; 51pp; English.
 PS
 CC The present sequence represents a murine interleukin-18 (IL-18)
 CC polypeptide. Interleukin-18 is a type of cytokine which mediates signal
 CC transduction in immune systems. The interleukin-18 receptor polypeptide
 CC can be used to neutralise interleukin-18 activity or to treat
 CC interleukin-18 receptor susceptible diseases, especially to treat
 CC autoimmune or allergic diseases or as an immunosuppressant. Conditions
 CC which may be treated include e.g. graft or organ rejection, pernicious
 CC anaemia, insulin-related diabetes, discoid lupus erythematosus,
 CC ulcerative colitis, hyperthyroidism, auto-immune hepatitis, systemic
 CC scleroderma, polyomyelitis, leukaemia, rheumatoid arthritis, HIV
 CC infections, asthma, atopic dermatitis, and pollinosis. The products may
 CC also be useful in the treatment of septic shock associated with
 CC IFN-alpha.
 XX
 SQ Sequence 157 AA:
 Query Match 99.8%; Score 806; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NFGRLHCTTAVIRNINDQVLFVDRKQVPEEDMDIDQASASEPQRLIITYMKDSEVRGLA 60
 DB 1 nfgrlhcttavrindqvlfvdkrqpvedmdidqasasepqrllitymkdsevrghla 60
 QY 61 VTLTVSKSKXSTLSCKNKIISFEEMDPENIDIDQSLIFPQKRVPGHNKMEFESSLYEG 120
 DB 61 vtltsvkkskstlscnklisfeemdpennididqsliffqkrvpgnkmefesslyeg 120
 QY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLLNLHQS 157
 DB 121 hflacqkedafrklilkkkdengdksvmtllnlhqs 157
 RESULT 7
 W63811
 ID W63811 standard; Protein; 157 AA.
 AC W63811;
 XX
 DT 28-SEP-1998 (first entry)
 XX
 DE Mouse IL-18 protein fragment.
 XX
 KM Interleukin-18; IL-18; murine; treatment; autoimmune disease; antibody;
 KM immunosuppressant; inhibitor; receptor protein; detection.
 KM
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..157
 FT /label= IL-18
 FT /note="partial sequence"
 FT Misc-difference 69 /label= Met or Thr
 FT
 XX
 PN EP850952-A1.
 PD 01-JUL-1998.
 XX
 PF 23-DEC-1997; 97EP-0310555.
 XX
 PR 28-JUL-1997; 97JP-0215490.
 PR 26-DEC-1996; 96JP-0356426.
 PR 21-FEB-1997; 97JP-0052526.
 PR 06-JUN-1997; 97JP-0163490.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Kunikata T, Kurimoto M, Torigoe K, Ushio S;
 PI
 XX
 DR MPI: 1998-335317/30.
 XX
 XX
 PT New interleukin-18 receptor protein used to inhibit interleukin-18,
 PT to treat autoimmune disease and as immunosuppressant - and new
 PT monoclonal antibody and hybridoma used to detect interleukin-18
 PT receptor protein
 XX
 PS Claim 5: Page 16-17; 35pp; English.
 XX
 CC This sequence represents a mouse interleukin-18 (IL-18) fragment which is
 CC used in a method involved in neutralising IL-18 or to treat autoimmune
 CC diseases or as an immunosuppressant using anti-IL-18 antibodies which
 CC can inhibit IL-18. Such antibodies can also be used to detect the IL-18
 CC receptor protein (labeled with an enzyme or a radioactive or fluorescent
 CC substance). The protein is used to treat e.g. graft rejection, pernicious
 CC anaemia, atrophic gastritis, insulin-resistant diabetes, Wegener
 CC granulomatosis, discoid lupus erythematosus, ulcerative colitis,
 CC cold-agglutinin-related diseases, Goodpasture's syndrome, primary
 CC biliary cirrhosis, sympathetic ophthalmitis, hyperthyroidism, juvenile
 CC onset type diabetes, Sjogren syndrome, autoimmune hepatitis, autoimmune
 CC haemolytic anaemia, myasthenia gravis, systemic scleroderma, systemic
 CC lupus erythematosus, polyleptic cold haemoglobinuria, polymyositis,
 CC periarthritis nodosa, multiple sclerosis, Addison's disease, purpura
 CC haemorrhagica, Basedow's disease, leukopenia, Behcet's disease,
 CC climacterium praecox, rheumatoid arthritis, rheumatopyra, chronic
 CC thyroiditis, Hodgkin's disease, HIV, asthma, atopic dermatitis, allergic
 CC nasitis, pollinosis, aptoxin allergy and septic shock resulting from
 CC production or administration of excessive gamma-interferon (IFN-gamma).
 CC
 XX
 SQ Sequence 157 AA:
 Query Match 99.8%; Score 806; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NFGRLHCTFAVININDOVLFVDKROPVFEDMDIDQASSEPOTRLIYYKDSVEVGLA 60
 DB 1 nfgrlhctavirindovlfvdkrpvfedmdidqasasepttriliiymkdsvevrgla 60
 OY 61 VTLISVDKSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGHNKMEFESSLYEG 120
 DB 61 vtlisvdkskxstlscnkkisfeemdpennididqsdliiffqkrvpgnhkmeffesslyeg 120
 OY 121 HFLACQKEDDAFKLILKKKDDNGDKSVMTLTNLHQ 157
 DB 121 hflacqkeddafklllkkkdngdksvmftlnlhnhs 157
 RESULT 8
 ID Y39800 standard: Protein: 157 AA.
 XX
 AC Y39800;
 XX
 DT 29-NOV-1999 (first entry)
 XX
 DE Interleukin-18 receptor protein sequence fragment.
 XX
 KM Interleukin-18 receptor; IL-18; human; mouse; organ transplant rejection;
 KM IL-18 receptor sensitive disease; immune reaction; therapy.
 OS Mammalia.
 XX
 XX
 XX Key Location/Qualifiers
 FH MISC-difference 70
 FT /note- "unspecified amino acid"
 XX
 XX JP11240898-A.

PD 07-SEP-1999.
 XX
 XX 12-MAR-1998; 98JP-0078549.
 PE
 XX
 XX 12-MAR-1997; 97JP-0074697
 PR 28-JUL-1997; 97JP-0215488.
 PR 09-OCT-1997; 97JP-0291837.
 PR 26-DEC-1997; 97JP-0366908.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 DR MPI: 1999-555071/47.
 XX
 PT New polypeptide - useful against interleukin-18 receptor sensitive
 PT diseases
 XX
 PS Disclosure: Page 37-38; 41pp; Japanese.
 XX
 CC This sequence is a fragment of an interleukin-18 receptor (IL-18R) of the
 CC invention. The IL-18R sequences were isolated from human and mouse. The
 CC sequences can be used in drugs for treating IL-18 receptor sensitive
 CC disease, especially effective for the relief of rejection accompanied to
 CC organ transplantation and for the treatment and the prevention of various
 CC diseases caused by excessive immune reaction.
 CC
 XX
 SQ Sequence 157 AA:
 Query Match 99.8%; Score 806; DB 20; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NFGRLHCTFAVININDOVLFVDKROPVFEDMDIDQASSEPOTRLIYYKDSVEVGLA 60
 DB 1 nfgrlhctavirindovlfvdkrpvfedmdidqasasepttriliiymkdsvevrgla 60
 OY 61 VTLISVDKSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGHNKMEFESSLYEG 120
 DB 61 vtlisvdkskxstlscnkkisfeemdpennididqsdliiffqkrvpgnhkmeffesslyeg 120
 OY 121 HFLACQKEDDAFKLILKKKDDNGDKSVMTLTNLHQ 157
 DB 121 hflacqkeddafklllkkkdngdksvmftlnlhnhs 157
 RESULT 9
 ID Y44598 standard: Protein: 157 AA.
 XX
 AC Y44598;
 XX
 DT 04-APR-2000 (first entry)
 XX
 DE Mouse monomeric interleukin-18.
 XX
 KM Mouse interleukin-18; IL-18; anti-IL-18-antibody; immunopathies;
 KM inflammatory disorder; autoimmune disease; anti-allergic;
 KM anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
 KM anti-allergic; antipyretic.
 XX
 OS Mus musculus.
 XX
 XX
 XX Key Location/Qualifiers
 FH MISC-difference 70
 FT /label= Met, Thr
 XX
 XX EP974600-A2.
 XX
 XX 26-JAN-2000.
 PD
 PE 24-JUN-1999; 99EP-0304977.
 XX
 XX 24-JUN-1998; 98JP-0177580.

PR 12-OCT-1998; 98JP-0289044.
 PR 22-DEC-1998; 98JP-0365023.
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;
 XX WPI: 2000-118341/11.
 XX
 PR New artificially produced peptide for neutralizing biological activity
 PT of interleukin-18, useful for treating and preventing immunopathies,
 PT inflammatory disorders and autoimmune diseases -
 XX
 PS Disclosure; Page 27; 32pp; English.
 CC The present sequence is mouse monomeric interleukin-18. This can comprise
 CC a part or the whole of the variable region in anti-interleukin-18
 CC -antibody for neutralising interleukin-18. This is useful for treating
 CC and preventing immunopathies, inflammatory disorders and autoimmune
 CC diseases which are caused by excessive immunoreaction. The protein has
 CC anti-allergic, anti-inflammatory, immunosuppressive, hematopoietic,
 CC leukocytopenic, antialgic, antipyretic and hepatic-function improving
 CC activities.
 CC
 SO Sequence 157 AA:
 QY
 Query Match 99.8%; Score 806; DB 21; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NGRRLCTAVIRNINDQVLFVDRKQPVFEDMTDIDQASSEPQTRLIIYMKDSEVRGLA 60
 DB 1 ngrlhtctavirndqvlfvdkrpvfedmtidqassepqtrliiymkdsevrsla 60
 QY 61 VLSVDSKXSTLSCKNKIISEFEMDPENIDIOSDLFFQKRVPGHNMKEFESSLYEG 120
 DB 61 vlsvdsksxstlscknkisfeemdpennididqsdliifqkrvpgnhknefesslyeg 120
 QY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNHHOS 157
 DB 121 hflacqkeddafklllkkkdengdksvmtltnhbs 157
 RESULT 10
 Y53905
 ID Y53905 standard; Protein: 157 AA.
 AC Y53905;
 XX
 DT 13-MAR-2000 (first entry)
 XX
 DE Amino acid sequence of a protein that induces IFN-gamma production.
 XX
 KW Mouse; interferon gamma production; IFN-gamma; immunocompetent cell;
 KW antiviral; immunoregulatory; antigen; mitogen;
 KW IFN-gamma susceptible disease; antibacterial; antitumor;
 KW AIDS; bacterial disease; candidiasis; malaria; solid malignant tumour;
 KW renal cancer; mycosis fungoides; chronic granulomatous disease;
 KW blood cell malignant tumour; adult T cell leukaemia;
 KW chronic myelogenous leukaemia; malignant leukaemia; immune disease;
 KW allergy; rheumatism.
 KW
 XX
 AC Mus sp.
 XX
 OS
 FT Key Location/Qualifiers
 FT Misc-difference 70 /note= "unspecified residue encoded by AYC"
 FT
 XX EP962531-A2.
 XX
 PD 08-DEC-1999.

XX
 XX 10-NOV-1995; 99EP-0104104.
 XX
 PF
 PR 15-NOV-1994; 94JP-0304203.
 PR 23-FEB-1995; 95JP-0058340.
 PR 10-MAR-1995; 95JP-0078357.
 PR 18-SEP-1995; 95JP-0262062.
 PR 29-SEP-1995; 95JP-0274988.
 PR 10-NOV-1995; 95EP-0308055.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 XX Ushio S, Torigoe K, Tanimoto T, Okamura H;
 PI
 DR WPI: 2000-064289/06.
 DR N-PSDB: 236923.
 DR
 XX
 XX Novel polypeptides used in the treatment of interferon-gamma
 PT susceptible diseases -
 XX
 PS Disclosure; Page 3; 42pp; English.
 CC The present sequence represents a murine protein that induces interferon
 CC (IFN)-gamma production by immunocompetent cells. IFN-gamma is a
 CC protein which has antiviral, antitumor and immunoregulatory activities,
 CC and is produced by immunocompetent cells stimulated with antigens or
 CC mitogens. A probe derived from the cDNA of the present sequence was used
 CC to isolate the corresponding human protein from human liver cells. The
 CC protein of the invention is used to treat IFN-gamma susceptible diseases,
 CC and also have use as a antiviral agent, antibacterial agent, antitumor
 CC agent, immunoregulatory agent and blood platelet enhancing agent.
 CC Diseases which can be treated with the protein include viral diseases
 CC such as hepatitis, herpes syndrome, condyloma, and AIDS; bacterial
 CC diseases such as candidiasis and malaria; solid malignant tumours such
 CC as renal cancer, mycosis fungoides and chronic granulomatous disease;
 CC blood cell malignant tumours such as adult T cell leukaemia, chronic
 CC myelogenous leukaemia, and malignant leukaemia; and immune diseases
 CC such as allergy and rheumatism.
 CC
 SO Sequence 157 AA:
 QY
 Query Match 99.8%; Score 806; DB 21; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NGRRLCTAVIRNINDQVLFVDRKQPVFEDMTDIDQASSEPQTRLIIYMKDSEVRGLA 60
 DB 1 ngrlhtctavirndqvlfvdkrpvfedmtidqassepqtrliiymkdsevrsla 60
 QY 61 VLSVDSKXSTLSCKNKIISEFEMDPENIDIOSDLFFQKRVPGHNMKEFESSLYEG 120
 DB 61 vlsvdsksxstlscknkisfeemdpennididqsdliifqkrvpgnhknefesslyeg 120
 QY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNHHOS 157
 DB 121 hflacqkeddafklllkkkdengdksvmtltnhbs 157
 RESULT 11
 Y57571
 ID Y57571 standard; protein: 157 AA.
 AC Y57571;
 XX
 OS
 DT 06-MAR-2000 (first entry)
 XX
 DE Murine interleukin 18 protein sequence SEQ ID NO.2.
 XX
 KW Murine; interleukin 18; IL-18; potentiator; IGF; tumour; cancer;
 KW interferon-gamma-inducing factor; growth inhibition; cyostatic.
 KW
 XX
 PD Mus sp.

XX MO959565-A1.
 XX 25-NOV-1999.
 PD 20-MAY-1999; 99WO-US1160.
 PF 21-MAY-1998; 98US-0086560.
 PR (SMIK) SMITHKLINE BEECHAM CORP.
 XX Johnson RK;
 PI WPI: 2000-062368/05.
 DR New polypeptides, useful for preparation of composition for preventing
 PT and/or treating cancer by inhibiting tumor growth
 PS Claim 2; Page 50; 53pp; English.
 XX The present sequence represents murine interleukin 18 (IL-18). The
 CC present invention describes a compound comprising human or murine IL-18
 CC in combination with a chemotherapeutic agent (I). Also described are:
 CC (1) a method of preventing and/or treating cancer in a mammal comprising
 CC the administration of a cancer inhibiting amount of (I) comprising the
 CC IL-18 protein and the chemotherapeutic agent and optionally a
 CC pharmaceutically acceptable carrier; and (2) a method of inhibiting the
 CC growth of tumor cells in a mammal sensitive to a composition comprising
 CC human IL-18 and/or murine IL-18 and the chemotherapeutic agent (and
 CC optionally a pharmaceutically acceptable carrier), comprising
 CC administering to a mammal afflicted with the tumor cells an effective
 CC amount of growth inhibiting amount of (I). The IL-18 protein in
 CC conjunction with a chemotherapeutic agent is useful in a method for
 CC preventing and/or treating cancer in mammals by inhibiting the growth
 CC of tumours or cancerous cells in mammals.
 XX Sequence 157 AA;
 SQ
 Query Match 99.8%; Score 806; DB 21; Length 157;
 Best Local Similarity 99.4%; Pred. No. 6.2e-79;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NFGRLHCTAVIRININDOVLFDVKROPVEEDMTIDIOSASBPOTRLIYWKDSEVGIA 60
 Db 1 nfgrlhctavirindovlfdvkrpveedmtidogsasepqrlllymkdsevgia 60
 QY 61 VTLGVKDSKXSTLCKNKKIISFEEMDPENIDIOSDLIFQKRVPGHNKMEFSSLYEG 120
 Db 61 vtlsvkdsksmtlscnkklisfeemdpennididsdliffqkrvpgnhkmeffesslyeg 120
 QY 121 HFLACQKEDDAFKLILKKKDKGSKSVFTLTNHHQS 157
 Db 121 hflacqkeddafkllkkkdengdksvmftltlnhqs 157
 RESULT 12
 W48960
 ID W48960 standard; Peptide; 180 AA.
 AC W48960;
 XX 25-SEP-1998 (first entry)
 DT Wild-type mouse interferon-gamma inducing factor.
 XX Interferon-gamma inducing factor; interferon-gamma; killer cell;
 KW antitumor agent; antiviral agent; antimicrobial agent; tumour; mGIF;
 KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
 KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
 XX Mus sp.
 XX

FH Key Location/Qualifiers
 FT Peptide 1..23
 FT Protein /note- "Signal peptide"
 FT 24..180
 FT /note- "Mature mouse IGIF which is claimed by the
 FT inventors under claim 4 in the specification"
 XX EP845530-A2.
 PN 03-JUN-1998.
 PD 28-NOV-1997; 97EP-0309632.
 PE 14-NOV-1997; 97JP-0329715.
 PR 29-NOV-1996; 96JP-0330307.
 PR 21-JAN-1997; 97JP-0020906.
 XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PA Kurimoto M, Okamoto I, Yamamoto K;
 PI WPI: 1998-288747/26.
 DR N-PSDB; V32755.
 DR Mutants of interferon-gamma inducing polypeptide - useful as
 PT antitumour, antiviral, antimicrobial or anti-immunopathic agents
 PS Claim 4; pages 38-39; 59pp; English.
 XX The present sequence represents the wild-type mouse interferon-gamma
 CC inducing factor (mGIF). The invention provides for mutant human and
 CC mouse interferon-gamma inducing factors in which one or more cysteine
 CC residues are replaced with different residues at or away from the
 CC consensus sequences shown in W48956-W48958. The mutant mGIFs are
 CC capable of stimulating immunocompetent cells for the production of
 CC interferon-gamma and are claimed to be less toxic, more active and stable
 CC than the corresponding wild type mGIF. The mutant mGIFs are also
 CC claimed to enhance killer cell cytotoxicity and/or induce killer cell
 CC formation; and may therefore be useful as antitumour agents, antitumour
 CC immunotherapeutics, antiviral agents and antimicrobial agents. The
 CC mutant mGIFs are also claimed to be useful for treating hepatitis,
 CC acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid
 CC malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
 CC thrombopenia caused by radiation- and chemo-therapy.
 XX Sequence 180 AA;
 SQ
 Query Match 99.8%; Score 806; DB 19; Length 180;
 Best Local Similarity 99.4%; Pred. No. 7.5e-79;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NFGRLHCTAVIRININDOVLFDVKROPVEEDMTIDIOSASBPOTRLIYWKDSEVGIA 60
 Db 24 nfgrlhctavirindovlfdvkrpveedmtidogsasepqrlllymkdsevgia 83
 QY 61 VTLGVKDSKXSTLCKNKKIISFEEMDPENIDIOSDLIFQKRVPGHNKMEFSSLYEG 120
 Db 84 vtlsvkdsksmtlscnkklisfeemdpennididsdliffqkrvpgnhkmeffesslyeg 143
 QY 121 HFLACQKEDDAFKLILKKKDKGSKSVFTLTNHHQS 157
 Db 144 hflacqkeddafkllkkkdengdksvmftltlnhqs 180
 RESULT 13
 W77090
 ID W77090 standard; Peptide; 157 AA.
 AC W77090;
 XX 16-NOV-1998 (first entry)
 DT
 XX

DE Mouse interleukin 18 derivative 1.
 XX
 KW Mouse; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 KW osteoclastoma; Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 KW chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.
 XX
 OS Mus sp.
 XX
 PN EP861663-AZ.
 XX
 PD 02-SEP-1998.
 XX
 PF 24-FEB-1998; 98EP-0301352.
 XX
 PR 25-FEB-1997; 97JP-0055468.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
 DR WPI: 1998-448964/39.
 XX
 XX
 PT Use of interleukin-18 to inhibit osteoclast formation - in treatment
 PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 PT osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
 PT primary hyperthyroidism and osteoporosis
 PS Disclosure: Page 34; 56pp; English.
 XX
 CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 CC
 SO Sequence 157 AA:
 Query Match 98.6%; Score 797; DB 19; Length 157;
 Best Local Similarity 98.7%; Pred. No. 5.7e-78;
 Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 NFGRLHCTTAVIRINNOVLFDVKRQPVFEDMDIDQASAPQRLITYMKDSEVRGLA 60
 DB 1 nfgrlhcttavrinnvdlfdvkrqpvfedmdidqasasepqrllitymkdsevrsla 60
 OY 61 VTLVSVDKSKXSTLSCKNKIISFEEMDPENIDIDQSLIFFOKRVPGNKMEFESSLYEG 120
 DB 61 vtlvsvdkskxstlscnkkiisfeemdpennididqsliffqkrvpghnkmeffesslyeg 120
 OY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLNHS 157
 DB 121 hflacqkedafrklllkkkdehgdksvmftltlnhgs 157
 RESULT 14
 ID W48968 standard; Peptide: 157 AA.
 XX
 AC W48968;
 XX
 DT 25-SEP-1998 (first entry)
 DE Mutant mouse interferon-gamma inducing factor mIGIF/MU11.
 XX
 KW Interferon-gamma inducing factor; interferon-gamma; killer cell;
 KW antitumour agent; antiviral agent; antimicrobial agent; tumour; mIGIF;
 KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
 KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
 XX
 OS Mus sp.
 OS Synthetic.

XX
 EH Key Location/Qualifiers
 FT Misc-difference 7
 FT /note= "changed from Cys in wild-type to Ala in
 FT mutant"
 FT
 XX
 PN EP845530-AZ.
 XX
 PD 03-JUN-1998.
 XX
 PF 28-NOV-1997; 97EP-0309632.
 XX
 PR 14-NOV-1997; 97JP-0329715.
 PR 29-NOV-1996; 96JP-0333037.
 PR 21-JAN-1997; 97JP-0020906.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Kurimoto M, Okamoto I, Yamamoto K;
 DR WPI: 1998-288747/26.
 DR N-PSDB: VJ2632.
 XX
 PT Mutants of interferon-gamma inducing polypeptide - useful as
 PT antitumour, antiviral, antimicrobial or anti-immunopathic agents
 PS Claim 6; page 44; 59pp; English.
 XX
 CC The present sequence represents the mutant mouse interferon-gamma
 CC inducing factor mIGIF/MU11. The wild-type mouse interferon-gamma
 CC factor (mIGIF) sequence is shown in W48960. The invention provides for
 CC mutant human and mouse interferon-gamma inducing factors in which one
 CC or more cysteine residues are replaced with different residues at or away
 CC from the consensus sequences shown in W48956-W48958. The mutant mIGIFs
 CC are capable of stimulating immunocompetent cells for the production of
 CC interferon-gamma and are claimed to be less toxic, more active and stable
 CC than the corresponding wild type mIGIF. The mutant mIGIFs are also
 CC claimed to enhance killer cell cytotoxicity and/or induce killer cell
 CC formation, and may therefore be useful as antitumour agents, antitumour
 CC immunotherapeutics, antiviral agents and antimicrobial agents. The
 CC mutant mIGIFs are also claimed to be useful for treating hepatitis,
 CC acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid
 CC malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
 CC thrombopenia caused by radiation- and chemo-therapy.
 CC
 SO Sequence 157 AA:
 Query Match 98.6%; Score 797; DB 19; Length 157;
 Best Local Similarity 98.7%; Pred. No. 5.7e-78;
 Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 NFGRLHCTTAVIRINNOVLFDVKRQPVFEDMDIDQASAPQRLITYMKDSEVRGLA 60
 DB 1 nfgrlhcttavrinnvdlfdvkrqpvfedmdidqasasepqrllitymkdsevrsla 60
 OY 61 VTLVSVDKSKXSTLSCKNKIISFEEMDPENIDIDQSLIFFOKRVPGNKMEFESSLYEG 120
 DB 61 vtlvsvdkskxstlscnkkiisfeemdpennididqsliffqkrvpghnkmeffesslyeg 120
 OY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLNHS 157
 DB 121 hflacqkedafrklllkkkdehgdksvmftltlnhgs 157
 RESULT 15
 ID W77091 standard; Peptide: 157 AA.
 XX
 AC W77091;
 XX
 DT 16-NOV-1998 (first entry)
 DE

DE Mouse Interleukin 18 derivative 2.

XX
KM Mouse: Interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
XX Chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.
XX

OS Mus sp.

PN EP861663-A2.

PD 02-SEP-1998.

XX 24-FEB-1998; 98EP-0301352.

XX 25-FEB-1997; 97JP-0055468.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;

XX WPI; 1998-448964/39.

DR
XX
XX Use of Interleukin-18 to inhibit osteoclast formation - in treatment
PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
PT osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
XX primary hyperthyroidism and osteoporosis

PS Disclosure; Page 34-35; 56pp; English.

XX
XX Interleukin-18 (IL-18) or a functional equivalent can be used for
CC inhibition of osteoclast formation. IL-18 is used for treating or
CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
XX arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
XX osteoporosis.

XX Sequence 157 AA;

Query Match

98.58; Score 796; DB 19; Length 157;

Best Local Similarity 98.7%; Pred. No. 7.3e-78;
Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NFGRLHCTTAVIRNINOVLFVDRKOPVEEDMTIDIOSASEPOTRLIIVYWKDSEVRGLA 60

Db 1 nfgrlhcttavrindvldvdkirpvedmtdidgasepqtllilymkdservgla 60

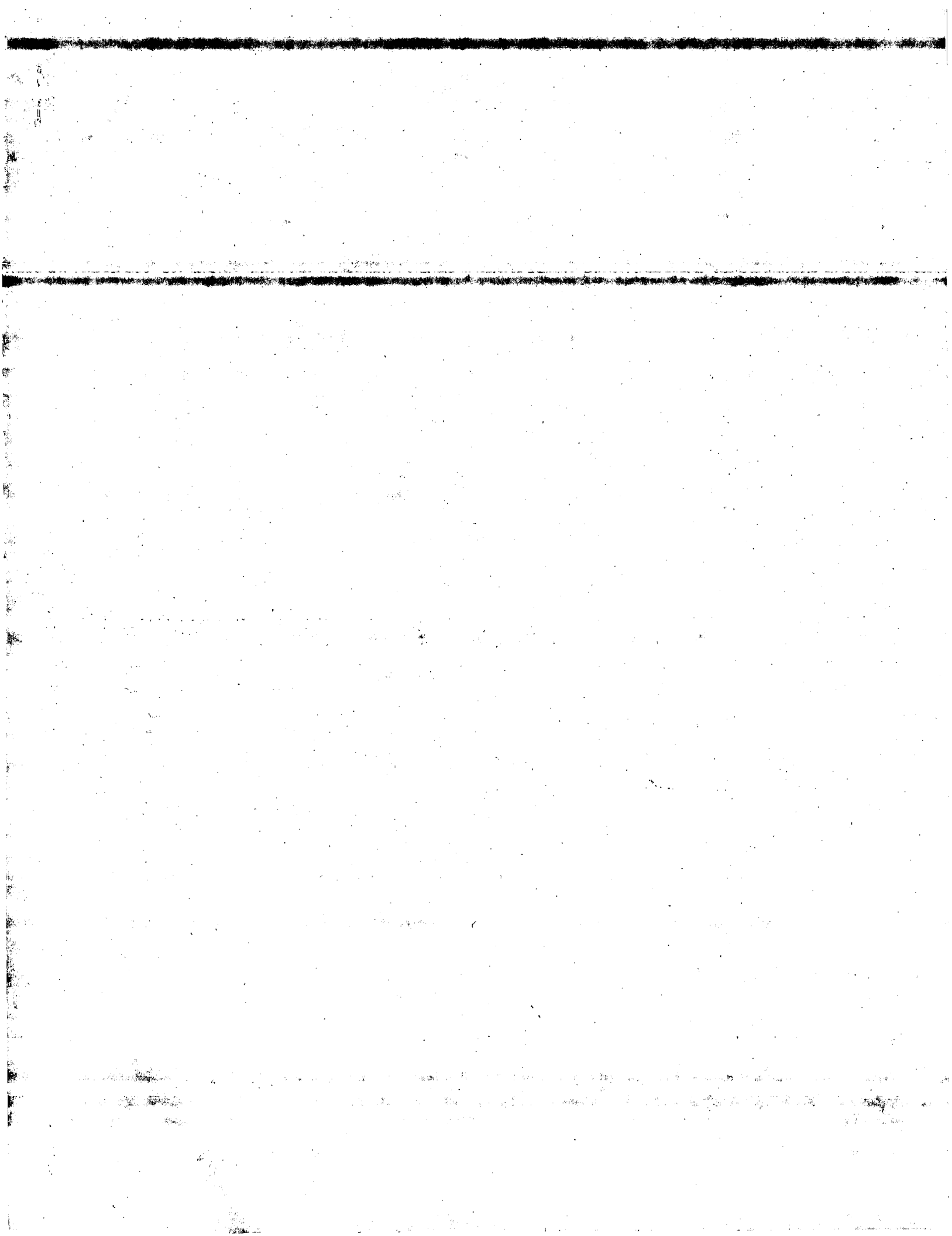
OY 61 VTLVKDSKXSTLSCKNKIISFEEMDPENIDIQSDLIFFQKRVPGHNKMEFESSLYEG 120

Db 61 vtlsvkdsksmtlscnkklisfeemdpennididqsdliifqkrvpghnmkfesslyeg 120

OY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTJNHQS 157

Db 121 hflasqkeddafkllkkkdengdksvmftltlnhqs 157

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Job time: 7373 sec



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OM protein - protein search, using sw model

Run on: November 21, 2000, 21:29:19 : Search time 25.82 seconds
(Without alignments)
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Gapop 10.0 , Gapext 0.5

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	806	99.8	157	2	US-08-502-535B-2
2	806	99.8	157	2	US-08-908-005A-12
3	806	99.8	157	3	US-08-996-338-27
4	513	63.5	157	2	US-08-896-605A-6
5	513	63.5	157	2	US-08-896-501A-14
6	513	63.5	157	3	US-08-884-324-1
7	513	63.5	157	3	US-08-896-338-26
8	513	63.5	193	2	US-08-896-605A-2
9	513	63.5	193	2	US-08-896-501A-2
10	80.5	10.0	456	1	US-08-464-164-2
11	80.5	10.0	456	1	US-08-338-057-2
12	80.5	10.0	456	1	US-08-668-416-2
13	76.5	9.5	1284	2	US-08-819-288-3
14	76.5	9.5	1321	1	US-08-261-822A-3
15	76.5	9.5	1321	4	PCT-US95-07744A-3
16	75.5	9.3	156	1	US-07-766-682A-3
17	74	9.2	269	1	US-08-203-716-3
18	74	9.2	269	1	US-08-440-179-3
19	74	9.2	269	2	US-08-432-693-11
20	74	9.2	269	2	US-08-489-895-11
21	74	9.2	269	2	US-08-483-806-2
22	74	9.2	269	3	US-09-211-290-11
23	74	9.2	269	3	US-09-030-613-11
24	74	9.2	269	3	US-09-322-676-11
25	74	9.2	269	4	PCT-US91-02339-1
26	74	9.2	1082	1	US-08-106-493A-2
27	74	9.2	1082	1	US-08-429-264-2
28	74	9.2	1139	1	US-08-832-883-2

29	74	9.2	1139	2	US-08-832-877-2	Sequence 2, Appl1
30	71.5	8.8	99	2	US-08-710-749-9	Sequence 9, Appl1
31	71	8.8	65	1	US-08-426-819A-33	Sequence 33, Appl1
32	71	8.8	248	1	US-08-426-819A-37	Sequence 37, Appl1
33	71	8.8	267	5	5494663-5	Patent No. 5494663
34	71	8.8	584	1	US-08-426-819A-36	Sequence 36, Appl1
35	71	8.8	622	1	US-08-426-819A-35	Sequence 35, Appl1
36	71	8.8	628	3	US-08-776-271-2	Sequence 2, Appl1
37	68.5	8.5	2509	1	US-08-469-005A-10	Sequence 10, Appl1
38	68	8.4	155	5	5494663-8	Patent No. 5494663
39	68	8.4	270	2	US-08-611-880-1	Sequence 1, Appl1
40	67.5	8.4	516	2	US-09-019-201A-3	Sequence 1, Appl1
41	67.5	8.4	866	1	US-08-100-692-1	Sequence 1, Appl1
42	67.5	8.4	866	2	US-08-674-030-1	Sequence 1, Appl1
43	67.5	8.4	874	2	US-08-247-904B-8	Sequence 8, Appl1
44	67.5	8.4	874	3	US-08-767-942A-21	Sequence 21, Appl1
45	67	8.3	153	5	521774-4	Patent No. 521774

ALIGNMENTS

RESULT 1
US-08-502-535B-2
Sequence 2, Application US/08502535B
Patent No. 5912324
GENERAL INFORMATION:
APPLICANT: OKAMURA, Haruki
APPLICANT: TANIMOTO, Tadao
APPLICANT: TORIGOE, Kakui
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND
TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,535B
FILING DATE: 14-JUL-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184162/1994
FILING DATE: 14-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 45057/1995
FILING DATE: 10-FEB-1995
AUTHOR/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKAMURA-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-502-535B-2

Query Match 99.8%; Score 806; DB 2; Length 157;

Best Local Similarity 100.0%; Pred. No. 2.4e-88;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGRLLCTTAVIRNINDQVLFVDRQPVFEDMTDIDQASSEPOTRLIIMYKDSVYRGLA 60
DB 1 NGRLLCTTAVIRNINDQVLFVDRQPVFEDMTDIDQASSEPOTRLIIMYKDSVYRGLA 60
QY 61 VLTLSVDSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGHNMFEESLYEG 120
DB 61 VLTLSVDSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGHNMFEESLYEG 120
QY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTFTLNHOS 157
DB 121 HFLACQKEDDAFKLILKKKDENGDKSVMTFTLNHOS 157

RESULT 2

US-08-908-005A-2

Sequence 2, Application US/08908005A

Patent No. 5914253

GENERAL INFORMATION:

APPLICANT: OKAMURA, Haruki

APPLICANT: TANIMOTO, Tadao

APPLICANT: TORIGOE, Kakuji

APPLICANT: KUNIKATA, Toshio

APPLICANT: TANIGUCHI, Mutsuko

APPLICANT: KOHNO, Keizo

APPLICANT: KURIMOTO, Masashi

TITLE OF INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND

TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,005A

FILING DATE: 11-AUG-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/502,535

FILING DATE: 14-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 184162/1994

FILING DATE: 14-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 45057/1995

FILING DATE: 10-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: OKAMURA=2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 157 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-908-005A-2

Query Match 99.8%; Score 806; DB 3; Length 157;

Best Local Similarity 100.0%; Pred. No. 2.4e-88;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGRLLCTTAVIRNINDQVLFVDRQPVFEDMTDIDQASSEPOTRLIIMYKDSVYRGLA 60
DB 1 NGRLLCTTAVIRNINDQVLFVDRQPVFEDMTDIDQASSEPOTRLIIMYKDSVYRGLA 60
QY 61 VLTLSVDSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGHNMFEESLYEG 120
DB 61 VLTLSVDSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGHNMFEESLYEG 120
QY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTFTLNHOS 157
DB 121 HFLACQKEDDAFKLILKKKDENGDKSVMTFTLNHOS 157

RESULT 3

US-08-996-338-27

Sequence 27, Application US/08996338

Patent No. 6087116

GENERAL INFORMATION:

APPLICANT: TORIGOE, Kakuji

APPLICANT: OKURA, Takao

APPLICANT: KURIMOTO, Masashi

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/996,338

FILING DATE: 22-DEC-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74,697/1997

FILING DATE: 12-MAR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 215,488/1997

FILING DATE: 28-JUL-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 291,837/1997

FILING DATE: 09-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: TORIGOE=3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 157

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-996-338-27

Query Match 99.8%; Score 806; DB 3; Length 157;

Best Local Similarity 100.0%; Pred. No. 2.4e-88;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Takanori OKURA
APPLICANT: Kakui TORIGOE
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-884-324-1

Query Match 63.5%; Score 513; DB 3; Length 157;
Best Local Similarity 64.9%; Pred. No. 1.6e-53;
Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;
QY 2 FGRHCTAVIRINDVLFVDK-RQPVFEDMTDIDQASSEPOTRLIITYMYKDSFVRGLA 60
DB 2 FGRHCTAVIRINDVLFVDK-RQPVFEDMTDIDQASSEPOTRLIITYMYKDSFVRGLA 60
QY 61 VTLVSKDKSKSTLSCNKKIISFEEDMPENIDDIOSDLIFPKRVPGH-NKNEFESSLYE 119
DB 62 VTLVSKDKSKSTLSCNKKIISFEEDMPENIDDIOSDLIFPKRVPGH-NKNEFESSLYE 119
QY 120 GHFLACQKEDDAFKLILKKKDEGDKSVAFETLTN 153
DB 122 GYFLACEKERDLFKLILKKKDEGDKSVAFETLTN 153

RESULT 7
US-08-996-338-26
Sequence 26, Application US/08996338
Patent No. 6087116
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakui
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 157
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-996-338-26

Query Match 63.5%; Score 513; DB 3; Length 157;
Best Local Similarity 64.9%; Pred. No. 1.6e-53;
Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;
QY 2 FGRHCTAVIRINDVLFVDK-RQPVFEDMTDIDQASSEPOTRLIITYMYKDSFVRGLA 60
DB 2 FGRHCTAVIRINDVLFVDK-RQPVFEDMTDIDQASSEPOTRLIITYMYKDSFVRGLA 60
QY 61 VTLVSKDKSKSTLSCNKKIISFEEDMPENIDDIOSDLIFPKRVPGH-NKNEFESSLYE 119
DB 62 VTLVSKDKSKSTLSCNKKIISFEEDMPENIDDIOSDLIFPKRVPGH-NKNEFESSLYE 119
QY 120 GHFLACQKEDDAFKLILKKKDEGDKSVAFETLTN 153
DB 122 GYFLACEKERDLFKLILKKKDEGDKSVAFETLTN 153

RESULT 8
US-08-896-605A-2
Sequence 2, Application US/08896605A
Patent No. 5879942
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30

Query Match	63.5%;	Score 513;	DB 2;	Length 193;
Best Local Similarity	64.9%;	Pred. No. 2.2e-53;		
Matches 100;	Conservative 26;	Mismatches 26;	Indels 2;	Gaps 2;

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QY      120 GHFLACQKEDDAFLILKKKDDENGDKSVMTILT 153
      1 : : : : : : : : : : : : : : : : : : : : : :
Db      158 GYFLACEKERDLFLKILKKEDDELGDRSIMFTVQN 191

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; sequence 2, Application US/08896501A
; Patent No. 5891663

ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington

MEDIUM TYPE: Floppy

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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: Patent In Release #1.0, Version #1.3C
;
; CURRENT APPLICATION DATA: 00.000.000

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; APPLICATION NUMBER: 05/08/896,501A
 ; FILING DATE: 18-JUL-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: ID 317 367/100

? APPLICATION NUMBER: JP 413,201/1996
 ? FILING DATE: 25-JUL-1996
 ?
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: JP 31,474/1997
 ? FILING DATE: 31-JAN-1997

Query Match	63.5%	Score 513;	DB 2;	Length 193;
Best Local Similarity	64.9%	Pred. No. 2.2e-53;		
Matches 100; Conservative	26;	Mismatches	26;	Indels 2; Gaps 2

QY 120 GHFLACQKEDDAFKLLKKDENGDKSVMEFTLTN 153
1:1:1:1:1 1:1:1:1:1 1:1:1:1:1 1
Db 158 GYFLACEKERDLFKLLKKEDELGDRSIMFTVON 191

RESULT 10
US-08-464-164-2

; sequence 2, Applicantroll US/08484184
; Patent No. 5614195
; Attorney: TROST & CO.

GENERAL INFORMATION:
APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Burnstead, Janene M.
APPLICANT: Vermellen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:

ADDRESS: Akzo No. 5614195el patent department
STREET: 1300 Piccard Drive, Suite 206

CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.

```

; ZIP: 20850
; COMPUTER READABLE FORM
;

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; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,164

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;; FILING DATE: June 2, 1995
;; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION
NAME: Gormley, Mary E.

REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 258-5200

SEQUENCE CHARACTERISTICS:

LENGTH: 450 amino acids
TYPE: amino acid
MODIFICATIONS: linear

MOLECULE TYPE: protein

US-08-4641-164-2

Query Match 10.0%; Score 80.5; DB 1; Length 456;
Best Local Similarity 25.7%; Pred. No. 0.19;
Matches 29; Conservative 21; Mismatches 42; Indels 21; Gaps 4;

OY 42 POTRLIIMYKDSEVRGLA---VTLVKDS-----KXSLSCNKKIISFEENDPPENI 91
DB 216 PQWRKVSSEPAKDLIRKMLAYVPSMRISAKDALDHPWIKSTDVYAKDSI-----NL 265
OY 92 DDIOSDLIFFQKRVPGHNMKEFESSLYEGHFLACQKEDDAFKLLKKDENG 144
DB 266 PSLESTILNT-RQFOGTOKLAALALYMGSKLTTNEETDELNKIFQKMDKNGD 317

RESULT 11

US-08-338-057-2
Sequence 2, Application US/08338057
Patent No. 5795741
GENERAL INFORMATION:
APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Bumstead, Janene M.
APPLICANT: Vermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Organon Teknika Corporation
STREET: 1330 Piccard Drive
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,057
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93.309078.9
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-338-057-2

Query Match 10.0%; Score 80.5; DB 1; Length 456;
Best Local Similarity 25.7%; Pred. No. 0.19;
Matches 29; Conservative 21; Mismatches 42; Indels 21; Gaps 4;

OY 42 POTRLIIMYKDSEVRGLA---VTLVKDS-----KXSLSCNKKIISFEENDPPENI 91
DB 216 PQWRKVSSEPAKDLIRKMLAYVPSMRISAKDALDHPWIKSTDVYAKDSI-----NL 265
OY 92 DDIOSDLIFFQKRVPGHNMKEFESSLYEGHFLACQKEDDAFKLLKKDENG 144
DB 266 PSLESTILNT-RQFOGTOKLAALALYMGSKLTTNEETDELNKIFQKMDKNGD 317

RESULT 12

US-08-668-416-2
Sequence 2, Application US/08668416
Patent No. 5843722

GENERAL INFORMATION:
APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Bumstead, Janene M.
APPLICANT: Vermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5843722e1 Patent Department
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,416
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/464,164
FILING DATE: June 2, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-668-416-2

Query Match 10.0%; Score 80.5; DB 2; Length 456;
Best Local Similarity 25.7%; Pred. No. 0.19;
Matches 29; Conservative 21; Mismatches 42; Indels 21; Gaps 4;

OY 42 POTRLIIMYKDSEVRGLA---VTLVKDS-----KXSLSCNKKIISFEENDPPENI 91
DB 216 PQWRKVSSEPAKDLIRKMLAYVPSMRISAKDALDHPWIKSTDVYAKDSI-----NL 265
OY 92 DDIOSDLIFFQKRVPGHNMKEFESSLYEGHFLACQKEDDAFKLLKKDENG 144
DB 266 PSLESTILNT-RQFOGTOKLAALALYMGSKLTTNEETDELNKIFQKMDKNGD 317

RESULT 13

US-08-619-288-3
Sequence 3, Application US/08819288
Patent No. 595652

GENERAL INFORMATION:
APPLICANT: Eckert, Joseph
APPLICANT: Alonso, Jose
TITLE OF INVENTION: PLANT GENES FOR SENSITIVITY TO ETHYLENE
TITLE OF INVENTION: AND PATHOGENS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 595652z15
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

TYPE: amino acid

Db 517 TTSTVTSYVDLPENILMTDOEIRSSPPEEELDVKYSTQ----VSSLKEDSDVKEQSV 571

Wed Nov 22 11:24:56 2000

us-09-050-249-2.ra1

Page 8

OY 62 TLS--VKDSKXSTLSCNNKIISEFENDPENIDDIQSOLIFFOKRVPG 107
DB 572 LOSTVNEVSODKDLIVETMAKIEPMSPEKIVSMENNSKFIKIDVEG 619

Search completed: November 21, 2000, 23:16:55
Job time: 6456 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 21, 2000, 21:31:49 ; Search time 42.57 Seconds

(without alignments)
234.044 Million cell updates/sec

Title: US-09-050-249-2

Perfect score: 808
Sequence: 1 NGRHLCTTAVIRININDVL.....KKDENGKSVMTFLTNLHOS 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	806	99.8	192	2	S60226 cytokine IGIF - mo
2	82.5	10.2	803	1	A64070 endopeptidase Ia (
3	82	10.1	267	1	JN0724 interleukin-1 beta
4	81	10.0	483	2	T21327 interleukin-1 prote
5	80.5	10.0	267	2	S38373 interleukin-1 beta
6	80	9.9	506	2	D71461 hypothetrical prote
7	79.5	9.8	526	2	A41698 cell division cont
8	78.5	9.7	1039	2	E72734 hypothetrical prote
9	78	9.7	1196	2	S46430 botulinum neurotox
10	78	9.7	1196	2	S46430 botulinum neurotox
11	78	9.7	1247	2	E71616 hypothetrical prote
12	77.5	9.6	366	2	T30457 interleukin-1 beta
13	77	9.5	266	1	ICB01B interleukin-1 beta
14	77	9.5	563	2	T09378 hypothetrical prote
15	76.5	9.5	167	2	A64401 hypothetrical prote
16	76.5	9.5	621	2	B64546 chaperone and heat
17	76.5	9.5	706	2	S38168 hypothetrical prote
18	76.5	9.5	905	2	T39572 probable proteins
19	76.5	9.5	1294	2	T48349 EIN2 protein - Ara
20	76	9.4	525	2	T43437 hypothetrical prote
21	75.5	9.3	270	1	ICM51 interleukin-1 alph
22	75.5	9.3	439	1	C64401 hypothetrical prote
23	75.5	9.3	626	2	T35669 hypothetrical ATP/G
24	75.5	9.3	695	2	F64135 carboxy-terminal p
25	75.5	9.3	866	2	T06454 probable lipoxigen
26	75	9.3	266	1	S23010 interleukin-1 beta
27	75	9.3	621	2	A11961 90kDa chaperone -
28	75	9.3	624	2	S67382 hypothetrical prote
29	75	9.3	1146	2	E70204 hypothetrical prote

30	74.5	9.2	270	1	S10532 interleukin-1 alph
31	74.5	9.2	661	2	S75005 sensory transducti
32	74	9.2	254	2	E70230 conserved hypothet
33	74	9.2	269	1	ICB01B interleukin-1 beta
34	74	9.2	318	2	C81447 chemotaxis protein
35	74	9.2	322	2	T48460 MADS-box protein-1
36	74	9.2	438	2	T45041 hypothetrical prote
37	74	9.2	1139	2	A49370 E1A-associated cyc
38	73.5	9.1	589	2	C72414 anthranilate synth
39	73.5	9.1	647	2	S61973 hypothetrical prote
40	73.5	9.1	680	2	T39858 hypothetrical prote
41	73.5	9.1	1146	2	T09112 probable sensor ki
42	73.5	9.1	2077	2	T43991 large tegument pro
43	73.5	9.1	2077	2	T44178 large tegument pro
44	73	9.0	611	2	S38162 translation elonga
45	73	9.0	872	1	P2XRCW RNA-binding protei

ALIGNMENTS

RESULT 1

S60226 cytokine IGIF - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000

C:Accession: S60226

R:Okamura, H.; Tautsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig

Nature 378, 88-91, 1995

A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.

A:Reference number: S60226; MUID:96061009

A:Accession: S60226

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-192 <OKA>

A:Cross-references: EMBL:D49949; NID:g1064822; PIDN:BAA08705.1; PID:g1064823

C:Superfamily: Mus musculus cytokine IGIF

Query Match

Best Local Similarity 99.8% Score 806; DB 2; Length 192;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy	1	NGRHLCTTAVIRININDVL	FVDRKOPVFEDMDIDDSASPPORLLIYWKDSEVGLA	60
Db	36	NGRHLCTTAVIRININDVL	FVDRKOPVFEDMDIDDSASPPORLLIYWKDSEVGLA	95
Oy	61	VTLSSVSKSKSTLSCNNKIISFEEMDPENIDIOSDLIFQKRVPGHNMKEFSSLYEG	120	
Db	96	VTLSSVSKSKSTLSCNNKIISFEEMDPENIDIOSDLIFQKRVPGHNMKEFSSLYEG	155	
Oy	121	HFLACQKEDDAFKLILKKKDKSGKSVMTFLTNLHOS	157	
Db	156	HFLACQKEDDAFKLILKKKDKSGKSVMTFLTNLHOS	192	

RESULT 2

A64070 endopeptidase Ia (EC 3.4.21.53) - Haemophilus influenzae (strain Rd KW20)

N:Alternate names: ARP-dependent proteinase Ipn; ARP-dependent serine proteinase Ia

C:Species: Haemophilus influenzae

C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 18-Jun-1999

C:Accession: A64070

R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman

; D.M.; Brandon, R.C.; Fine, L.D.; Fitchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Frazer, C.M.; Smith, H.O.; Vente

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630

A:Accession: A64070

A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-803 <TIGR>
 A:Cross-references: GB:U3729; GB:U42023; NID:q1573439; PIDN:AAC22121.1; PID:q1573440; T
 C:Comment: This allosteric enzyme catalyzes the hydrolysis of large proteins in the pres
 C:Gene(s):
 A:Gene: lon; lon-A
 C:Superfamily: ATP-dependent serine protease Ia
 C:Keywords: allosteric regulation; ATP; DNA binding; heat shock; hydrolase; P-loop; ser
 F:356-363/Region: nucleotide-binding motif A (P-loop)
 F:419-424/Region: nucleotide-binding motif B
 F:679/Active site: Ser #status predicted

Query Match 10.2%; Score 82.5; DB 1; Length 803;
 Best Local Similarity 18.9%; Pred. No. 10;
 Matches 44; Conservative 33; Mismatches 71; Indels 85; Gaps 7;

3 GRHCTAVIRIND--QVLFVDR-----QVFEDMTDIDOSAS-----40
 30 GRAKSIWALEAMNDKQILLVSQREADELEPTEDLEFDTGTTANITQLIKLPDPTVKVL 89
 41 -EPOTRIIIMYKDE-----VRGLAVTLVKDXXSTLSCNKIISFE 83
 90 VEQNRKIKSLDEGEKCSAQITPIETTYGDEKELVAKSAVSEPNLLIKKVPID 149
 84 EMPDENIDDI-----OSDLIFFOK 103
 150 ILNQLRIDVDRLADTMAHLPYSIRKONALELANVQERLEVLGLMSESDIIOVEK 209
 104 RVPGHNMKEFESSLYEGHFLACQEDAFLLIKKNDKDSVMTLTNHLQ 156
 210 RIRGRVKKOMEKS-QRNYVL-----NEQIKAIRKMDGENEDTIDEVEQLHQ 256

RESULT 3
 JN0724
 Interleukin-1 beta precursor - pig
 N:Alternate names: hematopoietin-1; IL-1 beta
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
 C:Accession: JN0724
 R:Huether, M.J.; Lin, G.; Smith, D.M.; Murtatugh, M.P.; Molitor, T.W.
 Gene 129, 285-289, 1993
 A:Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 be
 A:Reference number: JN0724; MUID:93314975
 A:Accession: JN0724
 A:Molecule type: mRNA
 A:Residues: 1-267 <HUE>
 A:Cross-references: GB:M86725; NID:q164607; PIDN:AAA02584.1; PID:q164608
 A:Experimental source: alveolar macrophage
 C:Comment: This protein is a pleiotropic cytokine that mediates a variety of processes
 C:Comment: This protein lacks a conventional signal sequence for protein export. Cleaved
 ved form of interleukin-1beta, unlike interleukin-1alpha, is inactive.
 C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
 C:Superfamily: interleukin-1
 C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
 F:115-267/Product: Interleukin-1 beta #status predicted
 F:77/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 10.1%; Score 82; DB 1; Length 267;
 Best Local Similarity 26.1%; Pred. No. 3.2;
 Matches 23; Conservative 22; Mismatches 31; Indels 12; Gaps 5;
 49 YMKSEVRGLAVTLVKDXXSTLSCNK-----IISFEMDP--PENIDDIOSDLIF 101
 160 FVQGDSDNNKIPVTLGIR-GKNLYLSCVMKDDIPTLOLEDIDPKRYPKR--DMERFVFY 216
 102 OKRVPGHNMKEFESSLYEGHFLACQED 129
 217 KTEI--KNRVEFESALYPNMYISTSOAE 242

RESULT 4
 T21327
 hypothetical protein F25C8.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T21327
 R:Matthews, L.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19407
 A:Accession: T21327
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-483 <WIL>
 A:Cross-references: EMBL:Z81512; PIDN:CAB04171.1; GSPDB:GN00023; CESP:F25C8.2
 A:Experimental source: clone F25C8
 C:Gene(s):
 A:Gene: CESP:F25C8.2
 A:Map position: 5
 A:Introns: 13/2; 136/2; 209/3; 358/3; 444/2

Query Match 10.0%; Score 81; DB 2; Length 483;
 Best Local Similarity 26.4%; Pred. No. 7.8;
 Matches 55; Conservative 24; Mismatches 63; Indels 66; Gaps 12;
 3 GRHCTAVIRINDV-----LFVDRQVFEEDMTDIDOSAS-----EPOTRII 48
 81 GTHFGAEVYVGVDEYVNYEKYDLF-DKTRKPTDDMLMDQDNTITLVNGHLVPRKIL 139
 49 YMKSEVRGLAVTLVKDXXSTLSCNKIIS--FEEN--DPENIDDIOSDLIFFOKRV 105
 140 DKFND-YIRYLVNVALYKSIKINQLSVENEINNOFIEFLRDPVPENDEIYSLINVKY- 196
 106 PGHNMKEFESSLYEGHFL-----ACQKEDA-----FKLIK 137
 197 --NYQTWSSPVGLSISLSTWDGTEEDSAVLNKGFEYELIKFRSKIRAGNRL 253
 138 -----KKDENGDSVMTLTN--LH 155
 254 NCEVINVKKEEN-----INWTLKNGEVLH 277

RESULT 5
 S38373
 Interleukin-1 beta precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
 C:Accession: S38373
 R:Van den Broeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; O
 Eur. J. Biochem. 217, 45-52, 1993
 A:Title: Gene sequence, cDNA construction, expression in Escherichia coli and genetic
 A:Reference number: S38373; MUID:94039070
 A:Accession: S38373
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-267 <VAN>
 A:Cross-references: EMBL:X74568; NID:q407899; PIDN:CAA52660.1; PID:q407900
 C:Gene(s):
 A:Introns: 16/2; 33/3; 99/1; 154/1; 197/3
 C:Superfamily: Interleukin-1

Query Match 10.0%; Score 80.5; DB 2; Length 267;
 Best Local Similarity 28.6%; Pred. No. 4.3;
 Matches 24; Conservative 22; Mismatches 25; Indels 13; Gaps 6;
 53 DSEVRGLAVTLVKDXXSTLSCNK-----IISFEMDP--PENIDDIOSDLIFFOKRV 105
 165 DSDDK-IPVTLGIR-GKNLYLSCVMKDDIPTLOLEDVDPKSTPKR--DMERFVFYKTEI 220
 106 PGHNMKEFESSLYEGHFLACQED 129

Db 221 --KNRYEFESALYPMNYISQAE 242

RESULT 6

D71461
hypothetical protein CT861 - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis

C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999

C:Accession: D71461

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis

A:Reference number: A71570; MUID:99000809

A:Accession: D71461

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-506 <ARN>

A:Cross-references: GB:AE001359; GB:AE001273; NID:g3329331; PIDN:AA66459.1; PID:g332933

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: CT861

Query Match 9.9%; Score 80; DB 2; Length 506;

Best Local Similarity 25.0%; Pred. No. 10;

Matches 38; Conservative 25; Mismatches 55; Indels 34; Gaps 7;

1 NGRHCTAVIRININDOVLFDKROPEVDMDDIDOSASEPOTRLIYMYKSEVAGLA 60

63 SFSRLQPTTP-----KERILFFGS-SPSSQLSSIVRTTSSPMN-----LFSNSQTNST 111

61 VTLVSVDKSKSTLCKN--KLIISPEMDPENIDDIQSDLIFFQKRVPGHNMKEFESSLY 118

112 RKISEKLFHSELSARSTKPSSEPIKPSENL-----LHTPEHKK-ELFSSLK 159

119 EGHFLACQKEDDAF-----KLIKKRDE 141

160 KDNLSPIMEIDFSFATESLEERLVQKKEE 191

Db 160 KDNLSPIMEIDFSFATESLEERLVQKKEE 191

RESULT 7

AA1698

cell division control protein CDC5 - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein G1345; protein YEL190c

C:Species: Saccharomyces cerevisiae

C:Date: 30-Jun-1992 #sequence_revision 18-Sep-1992 #text_change 29-Oct-1999

C:Accession: AA1698; S31274; S61128; S62055; S64207; S18513

R:Healy, A.M.; Zolnierowicz, S.; Stapleton, A.E.; Goebel, M.; Depaoli-Roach, A.A.; Pringle, Mol. Cell. Biol. 11, 5767-5780, 1991

A:Title: CDC5, a Saccharomyces cerevisiae gene involved in cellular morphogenesis: identification

A:Reference number: AA1698; MUID:92017858

A:Accession: AA1698

A:Molecule type: DNA

A:Residues: 1-526 <HEA1>

A:Cross-references: GB:M72716

A:Note: the authors translated the codon TAT for residue 116 as Val and COT for residue

R:Healy, A.M.; Zolnierowicz, S.; Stapleton, A.E.; Goebel, M.; Depaoli-Roach, A.A.; Pringle, submitted to the EMBL Data Library, July 1991

A:Reference number: S31274

A:Accession: S31274

A:Molecule type: DNA

A:Residues: 1-499, 'N', 501-526 <HEA2>

A:Cross-references: EMBL:M72716; NID:g171194; PIDN:AA34482.1; PID:g171195

R:Bertani, I.; Coglievina, M.; Zaccaria, P.; Klisma, R.; Brusch, C.V.

submitted to the EMBL Data Library, September 1995

A:Description: The sequence analysis of a 7.9 kb DNA fragment from the left arm of S.cerevisiae new genes.

A:Reference number: S61128

A:Accession: S61128

A:Molecule type: DNA

A:Residues: 1-281 <BER>

A:Cross-references: EMBL:X91489; NID:g1143557; PIDN:CA62785.1; PID:g199121; PID:g114355

R:Coglievina, M.; Delneri, D.; Zaccaria, P.; Klisma, R.; Bertani, I.; Brusch, C.V.

submitted to the EMBL Data Library, September 1995

A:Description: A 6.7 kb fragment from chromosome VII of Saccharomyces cerevisiae cont

A:Reference number: S62051

A:Accession: S62055

A:Molecule type: DNA

A:Residues: 283-526 <OCG>

A:Cross-references: EMBL:X91837; NID:g1177627; PIDN:CA62954.1; PID:e203624; PID:g117

A:Experimental source: strain FY1679

R:Brusch, C.V.; Coglievina, M.; Bertani, I.; Klisma, R.; Zaccaria, P.; Delneri, D.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S64183

A:Accession: S64207

A:Molecule type: DNA

A:Residues: 1-526 <BRU>

A:Cross-references: EMBL:Z72712; NID:g1322810; PIDN:CA696902.1; PID:e243794; PID:g132

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:CDG55

A:Cross-references: SGD:S0003158; MIPS:YGL190c

A:Map position: 7L

Query Match 9.8%; Score 79.5; DB 2; Length 526;

Best Local Similarity 25.0%; Pred. No. 12;

Matches 36; Conservative 29; Mismatches 56; Indels 23; Gaps 7;

14 NINDOVL-FVDRKQPEVDMDDIDOSASEPOTRLIYMYKSEVAGLAATLVSKSKXST 72

213 DIDQSFNIVIDIKPTMKELEVTSAERHPQCNLFMYSSK-----GIRKCDNRONS 267

73 LSCKNKIISFEEMDPENIDDIQSDLIFFQKRVPGHNMKEFESSLYEGHFLACQKEDDAF 132

268 L-CDNKTKEFEVLDLPINH-----FFPEIRTSIDIKFSN---GRYIASRD----- 311

133 KLILKKDENGSKSWFTLTINLQ 156

312 YLTWKIMDVNMNPKPLKTI-NIHE 334

Db 312 YLTWKIMDVNMNPKPLKTI-NIHE 334

RESULT 8

E72734

hypothetical protein 'APE0413 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 17-Mar-2000

C:Accession: E72734

R:Kawabata, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-uo, K.; Ta

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero

A:Reference number: A72450; MUID:99310339

A:Accession: E72734

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1039 <KAN>

A:Cross-references: DDBJ:AP000059; NID:g5103911; PIDN:BA479369.1; PID:d1043155; PID:g

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE0413

C:Superfamily: unassigned DEAD/H box helicases; DEAD/H box helicase homology

Query Match 9.7%; Score 78.5; DB 2; Length 1039;

Best Local Similarity 26.4%; Pred. No. 32;

Matches 37; Conservative 14; Mismatches 50; Indels 39; Gaps 5;

31 DMTDIDOSASEPOTRLIYMY-----YKSEVAGLAATLVSKSKXSTL 73

374 DIGEIDDELDEFEFLAIVDKLDDMFRELLKKAQYAAEDIVGKAV-----DSKVETL 428

74 SCRKKIISFEEMDPENIDDIQSDLIFFQKRVPGHNMKEFESSLYEGHFLACQKEDDAFK 133

429 --KILGLVLYPPPEELPDEFKDLA-SQKAIYFTEFKDAIYLYE-----K 471

Db 429 --KILGLVLYPPPEELPDEFKDLA-SQKAIYFTEFKDAIYLYE-----K 471

Db 91 NATVVYWNPIPIGEV----GVGDTRVFSVLTINDLFCNTMIIGHDIYSCVPEFRNVN 146

OY 119 EGHFLACQKEDDAFKLLKKDKDNGKSVMTL 151

Db 147 YKRLTRIEDPFLNLRLLRDDNNDFLLCKFL 179

RESULT 13

ICBO1B

Interleukin-1 beta precursor - bovine

N:Alternate names: hematopoietin-1; IL-1 beta

C:Species: Bos primigenius taurus (cattle)

C:Date: 31-Mar-1989 #sequence-revision 31-Mar-1989 #text-change 22-Jun-1999

C:Accession: J10010; S01380

R:Rajszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.; Moll, Immunol. 25, 429-437, 1988

A:Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin

A:Reference number: A94695; MID:88318652

A:Accession: J10010

A:Molecule type: mRNA

A:Residues: 1-266 <MAL>

A:Cross-references: GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201

R:Leong, S.R.; Flagg, G.M.; Lawman, M.; Gray, P.W.

Nucleic Acids Res. 16, 9054, 1988

A:Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.

A:Reference number: S01380; MID:89016591

A:Accession: S01380

A:Molecule type: mRNA

A:Residues: 1-251, 'A', 253-266 <LEDO>

A:Cross-references: EMBL:X12498; NID:g448; PIDN:CAA31018.1; PID:g449

C:Comment: This protein is a cytokine that mediates a variety of immunoregulatory and in

C:Comment: This protein lacks a conventional signal sequence for protein export. Cleaved

form of interleukin-1beta, unlike interleukin 1-alpha, is inactive

C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a

C:Superfamily: Interleukin-1

C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen

F:114-266/Product: Interleukin-1 beta #status predicted <MAT>

Query Match 9.5%; Score 77; DB 1; Length 266;

Best Local Similarity 26.0%; Pred. No. 8.9;

Matches 27; Conservative 24; Mismatches 33; Indels 20; Gaps 7;

OY 40 SEQOTRIIYMYKDESEK-----LAVTLVSDSKXSTLCKNK---LISFEEMP-- 87

Db 146 SQMNREVFPCM--SEVQGERDNKIPVALGICD-KNLYLSCVKKGPTPLQLEVDPKV 202

OY 88 -PENIDDIQSDLIFFOKRVPGNHKKMEFESSLYEGHFLACQKEDD 130

Db 203 YPKR--NMEKRVFYKTEI--KNITVEFSVLPYRWYISTQIEE 242

RESULT 14

T09378

hypothetical protein F23K16.250 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 11-Jun-1999 #sequence-revision 11-Jun-1999 #text-change 22-Oct-1999

C:Accession: T09378

R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, June 1999

A:Reference number: Z16652

A:Accession: T09378

A:Molecule type: DNA

A:Residues: 1-563 <BEV>

A:Cross-references: EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.250

A:Experimental source: cultivar Columbia; BAC clone F23K16

C:Genetics:

A:Gene: ATSP:F23K16.250

A:Map position: 4

A:Introns: 118/3; 502/3

Best Local Similarity 23.6%; Pred. No. 21;

Matches 33; Conservative 29; Mismatches 40; Indels 38; Gaps 7;

OY 22 VDKRPQVFEDMDIDOSAS--EPOTRIIYMYKDESEKGLAVLSKDS---KXSTLS- 74

Db 329 IDKAEWYFKKMNMDNYPISFTYECMIMMYGYGCSRRAREIEFEVGESESRVAKASTLA 388

OY 75 -----CKNKIISFEEMDPENIDDIQSDLIFFOKRVPGNHKKMF---ESSLYEGHFLAC 125

Db 389 MLEVYCRNGLY-----LEADKLF-----HNASAFRVHPDASTYKFLYKAY 428

OY 126 OKED--DAFKLLKKDKDENG 143

Db 429 TKADMKEQVQILKKMEKDG 448

RESULT 15

A64401

hypothetical protein M0809 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C:Date: 13-Sep-1996 #sequence-revision 13-Sep-1996 #text-change 22-Oct-1999

C:Accession: A64401

R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak

; Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weisslock, K.G.; Merrick, J.M.; Glodex,

ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc

A:Reference number: A64300; MID:96337999

A:Accession: A64401

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-167 <BUL>

A:Cross-references: GB:U67525; GB:L77117; NID:g1591497; PIDN:AA898817.1; PID:g1499632

C:Genetics:

A:Map position: FOR733027-733530

Query Match 9.5%; Score 76.5; DB 2; Length 167;

Best Local Similarity 26.8%; Pred. No. 5.7;

Matches 33; Conservative 16; Mismatches 39; Indels 35; Gaps 5;

OY 47 IIVMYKDESEKGLAVTLVSKD-----XSTLCKNKIISFEEMP--PENID 92

Db 38 IIVMYKDESEKGLAVTLVSKD-----XSTLCKNKIISFEEMP--PENID 92

OY 93 DIQSDLIFFOKRVPGNHKKMEFESSLYEGHFLACQKEDDAFKLLKKDKDNGKSVMTLT 152

Db 98 RLSSDDI-----LELNKKLDEG-----VKYIKLIFALEEH--KKVLLLEIK 136

OY 153 NLH 155

Db 137 DMH 139

Search completed: November 21, 2000, 23:19:59

Job time: 6490 sec

Query Match 9.5%; Score 77; DB 2; Length 563;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 21, 2000, 23:16:19 ; Search time 32.92 Seconds

(without alignments)
152.364 Million cell updates/sec

Title: US-09-050-249-2

Perfect score: 808
1 NEGRHCTTAVIRININDOVL.....KKDENGDKSVMTFLTNLHQS 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	806	99.8	192	1	IL18_MOUSE
2	736.5	91.2	194	1	IL18_RAT
3	538	66.6	193	1	IL18_HORSE
4	518	64.1	193	1	IL18_HUMAN
5	510	63.1	193	1	IL18_CANFA
6	509	63.0	192	1	IL18_PIG
7	82.5	10.2	803	1	LON_HAEN
8	82	10.1	267	1	ZABA_YEAST
9	79.5	9.8	526	1	IL1B_BOVIN
10	78	9.7	1196	1	EXCN_CLOBO
11	77	9.5	885	1	UE3A_MOUSE
12	76.5	9.5	167	1	Y809_JENJA
13	76.5	9.5	621	1	HTPG_HELPY
14	76.5	9.5	706	1	YK70_YEAST
15	76.5	9.4	269	1	IL1B_MACMU
16	76	9.4	268	1	IL1B_MACNE
17	75.5	9.3	270	1	IL1A_MOUSE
18	75.5	9.3	439	1	Y811_JENJA
19	75.5	9.3	695	1	PRC_HAEN
20	75.5	9.3	265	1	IL1B_SHEEP
21	75	9.3	268	1	IL1B_MACFA
22	75	9.3	624	1	YBY3_SCHPO
23	74.5	9.2	270	1	IL1A_PIG
24	74	9.2	269	1	IL1B_HUMAN
25	74	9.2	1139	1	RBL2_HUMAN
26	73.5	9.1	589	1	TRPG_THEMA
27	73	9.0	611	1	HBS1_YEAST
28	73	9.0	872	1	VP2_EOTPC
29	72.5	9.0	698	1	YB06_YEAST
30	72.5	9.0	1010	1	WNT5_DROME
31	72	8.9	207	1	ATPF_MYCPN
32	72	8.9	266	1	IL1B_CEREL
33	72	8.9	266	1	IL1B_CEREL

34	71.5	8.8	279	1	ATND_CAVPO
35	71.5	8.8	1215	1	ATG6_YEAST
36	71	8.8	165	1	HSCB_BUCAP
37	71	8.8	541	1	601M_HAEN
38	71	8.8	628	1	MSIN_HUMAN
39	71	8.8	1547	1	TOP2_BOMO
40	70.5	8.7	688	1	EFG_MYCPN
41	70.5	8.7	781	1	YB68_SCHPO
42	70	8.7	270	1	IL1A_FELCA
43	70	8.7	527	1	RAG2_MOUSE
44	70	8.7	747	1	AMD1_RAT
45	70	8.7	1381	1	YBE7_YEAST

ALIGNMENTS

RESULT 1
ID IL18_MOUSE STANDARD: PRT; 192 AA.
AC P70380:
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
GN IL18 OR IGIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=LIVER;
RX MEDLINE: 96061009.
RA Okamura H., Tsutsumi H., Komatsu T., Yutsudo M., Hakura A.,
RA Tanimoto T., Toriige K., Okura T., Nukada Y., Hattori K.,
RA Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.,
RT "Cloning of a new cytokine that induces IFN-gamma production by T
RT cells.";
RL Nature 378:88-91(1995).
RN [2]
RP SEQUENCE OF 1-191 FROM N.A.
RC STRAIN=NOD; TISSUE=PANCREAS;
RX MEDLINE: 97174346.
RA Rothe H., Jenkins N.A., Copeland N.G., Kolb H.,
RT "Active stage of autoimmune diabetes is associated with the
RT expression of a novel cytokine, IGIF, which is located near Idd2.";
RL J. Clin. Invest. 99:469-474(1997).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D49949; BAA08705.1; -;
DR EMBL: U66244; AAB49753.1; -;
DR MGD: MGI:107936; IL18.
KW Cytokine.
FT PROPEP 1 35
FT CHAIN 36 192 INTERLEUKIN-18.
FT CONFUCT 183 185 MFT -> IS (IN REF. 2).
SQ SEQUENCE 192 AA: 22135 MM: 8FED938473874D63 CRC64:
Query Match 99.8%; Score 806; DB 1; Length 192;

Best Local Similarity 99.4%; Pred. No. 7, 1e-67;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NGRHCTTAIVIRININDOVLFDKRPVFEEDMTIDQASASEPOTRLIITYMYKDESEVGLA 60
DB 36 NGRHCTTAIVIRININDOVLFDKRPVFEEDMTIDQASASEPOTRLIITYMYKDESEVGLA 95
QY 61 VTLVSXDSKXSTLSCKNKIISFEEMDPENIDIOSDLIFFOKRVPGHNMKEFESSLYE 120
DB 96 VTLVSXDSKXSTLSCKNKIISFEEMDPENIDIOSDLIFFOKRVPGHNMKEFESSLYE 155
QY 121 HFLACQKEDDAFKLILKKKDENGKSVAFITLNLHOS 157
DB 156 HFLACQKEDDAFKLILKKKDENGKSVAFITLNLHOS 192

RESULT 2

IL18_RAT STANDARD: PRT: 194 AA.

AC P97636: P97637: 088749;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
GN IL18 OR IGIF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]
RP SEQUENCE FROM N.A.
RX STRAIN-SPRAGUE-DAWLEY: TISSUE-ADRENAL GLAND:
MEDLINE: 97152963;
RA Conti B., Jahng J.W., Tanti C., Son J.H., Joh T.H.;
RT "Induction of Interferon-gamma inducing factor in the adrenal cortex";
RN J. Biol. Chem. 272:2035-2037(1997).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY: TISSUE-BRAIN;
RA Culhane A.C., Hall M.D., Rothwell N.J., Luheshi G.N.;
RT "Cloning of rat brain interleukin-18 cDNA";
RN Mol. Psych. 3:362-366(1998).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CELLS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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CC EMBL: 077776; AAC53009.1;
DR EMBL: 077777; AAC53010.1;
DR EMBL: AJ22813; CA11001.1;
KW Cytokine; Alternative splicing.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 194 INTERLEUKIN-18.
FT VARSPLIC 121 139 MISSING (IN ISOFORM ALPHA).
FT CONFLICT 4 5 MS -> IP (IN REF. 2).
FT CONFLICT 48 48 I -> M (IN REF. 2).
SQ SEQUENCE 194 AA: 22303 MW: E2089AD6F1798450 CRC64;

Query Match 91.2%; Score 736.5; DB 1; Length 194;
Best Local Similarity 89.9%; Pred. No. 1.6e-60;
Matches 142; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

QY 1 NGRHCTTAIVIRININDOVLFDKRPVFEEDMTIDQASASEPOTRLIITYMYKDESEVGL 59
DB 37 NGRHCTTAIVIRININDOVLFDKRPVFEEDMTIDQASASEPOTRLIITYMYKDESEVGL 96
QY 60 VTLVSXDSKXSTLSCKNKIISFEEMDPENIDIOSDLIFFOKRVPGHNMKEFESSLYE 119
DB 97 VTLVSXDSKXSTLSCKNKIISFEEMDPENIDIOSDLIFFOKRVPGHNMKEFESSLYE 156
QY 120 HFLACQKEDDAFKLILKKKDENGKSVAFITLNLHOS 157
DB 157 HFLACQKEDDAFKLILKKKDENGKSVAFITLNLHOS 194

RESULT 3

IL18_HORSE STANDARD: PRT: 193 AA.

AC Q9XSQ7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
GN IL18 OR IGIF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
[1]
RP SEQUENCE FROM N.A.
RA Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA Argyle D.J., Onions D.E.;
RT "Nucleotide sequence of equine interleukin 12 and 18 cDNAs";
RN Submitted (Feb-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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Query Match 66.6%; Score 538; DB 1; Length 193;
Best Local Similarity 68.8%; Pred. No. 2.1e-42;
Matches 106; Conservative 23; Mismatches 23; Indels 2; Gaps 2;

QY 2 NGRHCTTAIVIRININDOVLFDKRPVFEEDMTIDQASASEPOTRLIITYMYKDESEVGLA 60
DB 38 NGRHCTTAIVIRININDOVLFDKRPVFEEDMTIDQASASEPOTRLIITYMYKDESEVGLA 97
QY 61 VTLVSXDSKXSTLSCKNKIISFEEMDPENIDIOSDLIFFOKRVPGH-NKMEFESSLYE 119
DB 98 VTLVSXDSKXSTLSCKNKIISFEEMDPENIDIOSDLIFFOKRVPGH-NKMEFESSLYE 157
QY 120 HFLACQKEDDAFKLILKKKDENGKSVAFITLNLHOS 153
DB 158 HFLACQKEDDAFKLILKKKDENGKSVAFITLNLHOS 191

RESULT 4
IL18_HUMAN STANDARD: PRT: 193 AA.

AC Q14116; 075599;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
 DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
 GN IL18 OR IGIF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE: 96247646.
 RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
 Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
 Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
 RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
 RT in Escherichia coli, and studies on the biologic activities of the
 RT protein.";
 RL J. Immunol. 156:4274-4279(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yong D., Guixin D., Linhua H., Haitao W.;
 RT "Cloning and sequencing of the cDNA for precursor hIL-18.";
 RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 2-193 FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD;
 RA Corti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
 CC -----
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 CC -----
 CC EMBL: D49950; BAA08706.1;
 DR EMBL: AF077611; AAC27787.1;
 DR EMBL: U90434; AAB50010.1;
 DR MIM: 600953;
 DR Cytokine.
 KW PROPEP 1 36 BY SIMILARITY.
 CHAIN 37 193 INTERLEUKIN-18.
 FT CONFLICT 66 66 F -> L (IN REF. 2).
 FT CONFLICT 86 86 S -> R (IN REF. 2).
 FT CONFLICT 191 191 N -> S (IN REF. 2).
 SO SEQUENCE 193 AA: 22326 MW: 323C62C20378BD55 CRC64;

Query Match 64.1%; Score 518; DB 1; Length 193;
 Best Local Similarity 65.6%; Pred. No. 1.4e-40;
 Matches 101; Conservative 26; Mismatches 25; Indels 2; Gaps 2;

QY 2 FGRHCTAVININDVLFVOK-RQPVFEDMTDIDQASSEQTRLIIMYKDSVRGLA 60
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
 DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
 GN IL18 OR IGIF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE: 96247646.
 RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
 Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
 Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
 RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
 RT in Escherichia coli, and studies on the biologic activities of the
 RT protein.";
 RL J. Immunol. 156:4274-4279(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yong D., Guixin D., Linhua H., Haitao W.;
 RT "Cloning and sequencing of the cDNA for precursor hIL-18.";
 RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 2-193 FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD;
 RA Corti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
 CC -----
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 CC -----
 CC EMBL: D49950; BAA08706.1;
 DR EMBL: AF077611; AAC27787.1;
 DR EMBL: U90434; AAB50010.1;
 DR MIM: 600953;
 DR Cytokine.
 KW PROPEP 1 36 BY SIMILARITY.
 CHAIN 37 193 INTERLEUKIN-18.
 FT CONFLICT 66 66 F -> L (IN REF. 2).
 FT CONFLICT 86 86 S -> R (IN REF. 2).
 FT CONFLICT 191 191 N -> S (IN REF. 2).
 SO SEQUENCE 193 AA: 22326 MW: 323C62C20378BD55 CRC64;

RESULT 5
 ID IL18_CANFA STANDARD: PRT: 193 AA.
 AC Q9XSRO;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
 DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
 GN IL18 OR IGIF.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Argyle D.J., McGillivray C., Nicolson L., Onions D.E.;
 RT "Cloning, sequencing and characterization of canine interleukin-18.";
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
 CC -----
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 CC -----
 CC EMBL: Y11133; CAA72015.1;
 DR Cytokine.
 KW PROPEP 1 36 BY SIMILARITY.
 CHAIN 37 193 INTERLEUKIN-18.
 FT CONFLICT 37 193 INTERLEUKIN-18.
 SO SEQUENCE 193 AA: 22037 MW: 0D973E586F461F25 CRC64;

Query Match 63.1%; Score 510; DB 1; Length 193;
 Best Local Similarity 64.9%; Pred. No. 7.4e-40;
 Matches 100; Conservative 25; Mismatches 27; Indels 2; Gaps 2;

QY 2 FGRHCTAVININDVLFVOK-RQPVFEDMTDIDQASSEQTRLIIMYKDSVRGLA 60
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
 DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
 GN IL18 OR IGIF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE: 96247646.
 RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
 Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
 Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
 RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
 RT in Escherichia coli, and studies on the biologic activities of the
 RT protein.";
 RL J. Immunol. 156:4274-4279(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yong D., Guixin D., Linhua H., Haitao W.;
 RT "Cloning and sequencing of the cDNA for precursor hIL-18.";
 RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 2-193 FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD;
 RA Corti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
 CC -----
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 CC -----
 CC EMBL: D49950; BAA08706.1;
 DR EMBL: AF077611; AAC27787.1;
 DR EMBL: U90434; AAB50010.1;
 DR MIM: 600953;
 DR Cytokine.
 KW PROPEP 1 36 BY SIMILARITY.
 CHAIN 37 193 INTERLEUKIN-18.
 FT CONFLICT 66 66 F -> L (IN REF. 2).
 FT CONFLICT 86 86 S -> R (IN REF. 2).
 FT CONFLICT 191 191 N -> S (IN REF. 2).
 SO SEQUENCE 193 AA: 22326 MW: 323C62C20378BD55 CRC64;

Query Match 63.1%; Score 510; DB 1; Length 193;
 Best Local Similarity 64.9%; Pred. No. 7.4e-40;
 Matches 100; Conservative 25; Mismatches 27; Indels 2; Gaps 2;

QY 2 FGRHCTAVININDVLFVOK-RQPVFEDMTDIDQASSEQTRLIIMYKDSVRGLA 60
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
 DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
 GN IL18 OR IGIF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE: 96247646.
 RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
 Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
 Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
 RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
 RT in Escherichia coli, and studies on the biologic activities of the
 RT protein.";
 RL J. Immunol. 156:4274-4279(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yong D., Guixin D., Linhua H., Haitao W.;
 RT "Cloning and sequencing of the cDNA for precursor hIL-18.";
 RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 2-193 FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD;
 RA Corti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
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 CC CELLS.
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 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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 CC -----
 CC EMBL: D49950; BAA08706.1;
 DR EMBL: AF077611; AAC27787.1;
 DR EMBL: U90434; AAB50010.1;
 DR MIM: 600953;
 DR Cytokine.
 KW PROPEP 1 36 BY SIMILARITY.
 CHAIN 37 193 INTERLEUKIN-18.
 FT CONFLICT 66 66 F -> L (IN REF. 2).
 FT CONFLICT 86 86 S -> R (IN REF. 2).
 FT CONFLICT 191 191 N -> S (IN REF. 2).
 SO SEQUENCE 193 AA: 22326 MW: 323C62C20378BD55 CRC64;

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CC -1- FUNCTION: DEGRADATES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS
CC IN PRESENCE OF ATP. DEGRADATES THE REGULATORY PROTEINS PCSA AND
CC SUIA. HYDROLYZES TWO ATPs FOR EACH PEPTIDE BOND CLEAVED IN THE
CC PROTEIN SUBSTRATE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF LARGE PROTEINS SUCH AS GLOBIN,
CC CASEIN AND DENATURATED SERUM ALBUMIN, IN PRESENCE OF ATP.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOSOL;CYTOSOLIC.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16; ALSO KNOWN AS THE
CC LON FAMILY OF ATP-DEPENDENT PROTEASES.
CC -----
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CC -----
CC DR EMBL; U32729; AAC22121.1;
CC DR TIGR; H10462;
CC DR INTERPRO; IPR001939;
CC DR INTERPRO; IPR001984;
CC DR PFMAM; PFM00004; AAA; 1.
CC DR PRINTS; PRO0830; ENDOLAPTASE.
CC DR PROSITE; PS01046; LON_SER; 1.
CC KM Hydrolyase; Serine protease; ATP-binding
CC FT NP_BIND 356 363 ATP (POTENTIAL).
CC FT ACT_SITE 679 679 BY SIMILARITY.
CC SQ SEQUENCE 803 AA; 89347 MW; 9E590852611BEA5B CRC64;
CC -----
QY Query Match 10.28; Score 82.5; DB 1; Length 803;
QY Best Local Similarity 18.9%; Pred. No. 4.3;
QY Matches 44; Conservative 33; Mismatches 71; Indels 85; Gaps 7;
QY -----
QY 3 GRHCTTAVININD--OVLFDVDR--OPVFEDMTDIDQSAS----- 40
QY 30 GRAKSNALPEAMNDKCOLVLSQREADLEPTPDLDTVGITIANIIDLKLPDPTVAVL 89
QY 41 -EPQTRLIIYWKDSE-----VRLAVTLVSKDSKSTLCKNKRIISFE 83
QY 90 VEGQKRAKINSLEDEGEKFSAOITPIETTYGDEKELVAKSAVLSEFENYLTLNKKVPTD 149
QY 84 EMDPENTIDDI-----QSDLIFQK 103
QY 150 ILNALORIDVDRLADTMAAHLPSIRKONALELANYOERLEYLLGMSEADILQVER 209
QY 104 RVPGNKKKEFFESSLYEGHFLACOKEDDAFKLILKKKDENGSKSVAFITLNHQ 156
QY 210 RIRGRVKKQMKERS-QRNYL-----NEGIRKAIKREMDGEGENDRTIDEVQLHQ 256
QY -----
DB Db
DB ID IL1B_PIG STANDARD; PRT; 267 AA.
DB AC P26889;
DB DT 01-AUG-1992 (Rel. 23, Created)
DB DT 01-AUG-1992 (Rel. 23, Last sequence update)
DB DT 30-MAY-2000 (Rel. 39, Last annotation update)
DB DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
DB GN IL1B.
DB OS Sus scrofa (Pig).
DB OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
DB RN [1]
DB RP SEQUENCE FROM N.A.
DB RX MEDLINE; 93314975.
DB RA Huebner M.J., Lin G., Smith D.M., Murtough M.P., Mollitor T.W.;
DB RT "Cloning, sequencing and regulation of an mRNA encoding porcine
DB RT interleukin-1 beta."
DB RL Gene 129:285-289(1993).
DB CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES

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CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEIN ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC -1 SUBUNIT: MONOMER.
 CC -1 DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -1 MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -1 SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC -----
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 CC -----
 CC EMBL, M86725; AA02584.1; -
 CC PIR, JN0724; JN0724.
 CC HSSP, P01584; 1H1B.
 CC INTERPRO: IPR000975; -
 CC INTERPRO: IPR002348; -
 CC PFMAM, PF00340; Interleukin-1; 1.
 CC PRINTS: PF00262; IL1HBF.
 CC PRINTS: PR00264; INTERLEUKIN_1; 1.
 CC PROSITE: PS00253; INTERLEUKIN_1; 1.
 CC Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
 CC PROPEP 1 114 BY SIMILARITY
 CC CHAIN 115 267 INTERLEUKIN-1 BETA.
 CC SEQUENCE 267 AA; 30404 MW; 7EB92B784D5086F CRC64;
 SQ
 Query Match 10.1%; Score 82; DB 1; Length 267;
 Best Local Similarity 26.1%; Pred. No. 1.3; Indels 12; Gaps 5;
 Matches 23; Conservative 22; Mismatches 31;
 QY 49 VYKDESEVGLAVTISKXSTLSCNKK---IISFEMDP--PENIDIQSLDF 101
 DB 160 FVQGDSDNNKIKPTVLGK-GKNLYLSCVAKDMVPTLQLEDIDPKRYPKR--DMERKFRVY 216
 QY 102 QKRVPGHNKMFESSLYEGHFLACQKED 129
 DB 217 KTEI--KNRVEFESALYPMWYSTSOAE 242
 RESULT 9
 2ABA_YEAST STANDARD; PRT: 526 AA.
 ID 2ABA_YEAST
 AC 000362;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PROTEIN PHOSPHATASE PP2A REGULATORY SUBUNIT B (PR55) (CELL DIVISION
 DE CONTROL PROTEIN 55).
 GN CDC55 OR YGL190C OR G1345.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Saccharomyces.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92017858.
 RA Healy A.M., Zolnerowicz S., Stapleton A.E., Goebel M.,
 RA Despoil-Roach A.A., Pringle J.R.,
 RT "CDC55, a Saccharomyces cerevisiae gene involved in cellular
 RT morphogenesis: identification, characterization, and homology to the
 RT B subunit of mammalian type 2A protein phosphatase.",
 RL Mol. Cell. Biol. 11:5767-5780(1991).
 RN (2)

RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / FY1679;
 RX MEDLINE: 92167971.
 RA Cogolierna M., Klima R., Bertani I., Delneri D., Zaccaria P.,
 RA Brusch C.V.;
 RT "Sequencing of a 40.5 kb fragment located on the left arm of
 RT chromosome VII from Saccharomyces cerevisiae".
 RL Yeast 13:55-64(1997).
 CC -1 FUNCTION: PHOSPHATASE 2A AFFECTS A VARIETY OF BIOLOGICAL PROCESSES
 CC IN THE CELL, SUCH AS TRANSCRIPTION, CELL CYCLE PROGRESSION AND
 CC CELLULAR MORPHOGENESIS, AND PROVIDES AN INITIAL IDENTIFICATION OF
 CC CRITICAL SUBSTRATES FOR THIS PHOSPHATASE. THE REGULATORY SUBUNIT
 CC MAY DIRECT THE CATALYTIC SUBUNIT TO DISTINCT, ALBEIT OVERLAPPING,
 CC SUBSETS OF SUBSTRATES.
 CC -1 SUBUNIT: PP2A EXISTS IN SEVERAL TRIMERIC FORMS, ALL OF WHICH
 CC CONSIST OF A CORE COMPOSED OF A CATALYTIC SUBUNIT ASSOCIATED WITH
 CC A 65 KDA (PR55) (SUBUNIT A) AND A 55 KDA (PR55) (SUBUNIT B)
 CC REGULATORY SUBUNIT.
 CC -1 SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL, M72716; AA34482.1; -
 CC EMBL, 272712; CA96902.1; -
 CC EMBL, X91837; CA62954.1; -
 CC EMBL, X91489; CA62785.1; -
 CC PIR, A41698; A41698.
 CC SGD, S0003158; CDC35.
 CC INTERPRO: IPR000009; -
 CC PFMAM, PF01240; PR55; 1.
 CC PRINTS: PR00600; PP2APR55.
 CC PROSITE: PS01024; PR55_1; 1.
 CC PROSITE: PS01025; PR55_2; 1.
 CC Cell cycle.
 CC DOMAIN: 416 419 POLY-SER.
 CC CONFLICT 500 500 I->N (IN REF. 1).
 CC SEQUENCE 526 AA; 59662 MW; 6DA12C2805FA6A82 CRC64;
 SQ
 Query Match 9.8%; Score 79.5; DB 1; Length 526;
 Best Local Similarity 23.0%; Pred. No. 4.9;
 Matches 36; Conservative 29; Mismatches 56; Indels 23; Gaps 7;
 QY 14 NINDOVL-FVDRKQVFEEDMDIDQSASBPQRLTIYWKDSEVGLAVTISKXST 72
 DB 213 DIPDOSFNIVDKPTNMEELTIVTSAEFHPOECLFAYSSK-----GTILCDMRONS 267
 QY 73 LSCNKKIISFEMDPDENIDIQSLDFQKRVPGHNKMFESSLYEGHFLACQKEDAF 132
 DB 268 L-CDNKKTTFEEYLDPIHNH-----FFETITSSIDIKFSPN---GRYIASRD----- 311
 QY 133 KILKKKDEGDKSVFILTNDHQ 156
 DB 312 YLTVKIMVNMMDNKKPKIT-NIHE 334
 RESULT 10
 IL1B_BOVIN STANDARD; PRT: 266 AA.
 ID IL1B_BOVIN
 AC P09428;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
 RN IL1B
 OS Bos taurus (Bovine).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89016591.
 RA Leong S.R., Flaegs G.M., Lawman M., Gray P.W.;
 RT "The nucleotide sequence for the cDNA of bovine Interleukin-1 beta."
 RN Nucleic Acids Res. 16:9054-9054(1988).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 88318652.
 RA Maliszewski C.R., Baker P.E., Schoenborn M.A., Davis B.S., Cosman D.,
 RA Gillis S., Cerretti D.P.;
 RT "Cloning, sequence and expression of bovine Interleukin 1 alpha and
 RT Interleukin 1 beta complementary DNAs";
 RL Mol. Immunol. 25:429-437(1988).
 CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SINOVIAL CELLS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC -----
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 CC -----
 DR EMBL: M35589; AAA30585.1;
 DR EMBL: X12498; CAA31018.1;
 DR EMBL: M37211; AAA30584.1;
 DR PIR: JL0010; ICB01B.
 DR PIR: S01380; S01380.
 DR HSP: P01584; IIB.
 DR INTERPRO: IPR000975;
 DR INTERPRO: IPR002348;
 DR PRAM: PF00340; Interleukin-1; 1.
 DR PRINTS: PR00262; ILIHGF.
 DR PRINTS: PR00264; INTERLEUKIN1.
 DR PROSITE: PS00253; INTERLEUKIN1; 1.
 KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
 FT PROPEP 1 113
 FT CHAIN 1 266
 FT CONFLICT 252 252 INTERLEUKIN-1 BETA.
 FT CONFLICT 252 252 A -> G (IN REF. 2).
 SQ SEQUENCE 266 AA; 30774 MW; 9D1EF8F575070586 CRC64;

Query Match 9.88; Score 79; DB 1; Length 266;
 Best Local Similarity 27.58; Pred. No. 2.4;
 Matches 33; Conservative 18; Mismatches 33; Indels 36; Gaps 8;
 QY 40 SEPTRLIIVYKDEVRG-----LAVTLVSKSKXSTLSCNKK-----IISFEEMP-- 87
 DB 146 SQENNRREVFCM--SFVQGERDKKIPVAGLIRK-KNLVYLSGVKKGTPITLQLEEVVPKV 202
 QY 88 -PENIDDIQSDLIFFQKRVPGHNKMEFESSLYE-----GHFLACQKEDD 130
 DB 203 YPKR--NMKREVFYKTEI--KNTVEFESVLYPNWYISTQIEERPVLGHRFRAGQDITD 258

RESULT 11

BXCN_CLOBO
 ID BXCN_CLOBO STANDARD; PRT; 1196 AA.
 AC P46081;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE BOTULINUM NEUROTOXIN TYPE C1, NONTOXIC COMPONENT.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TYPE C STOCKHOLM / C-ST;
 RX MEDLINE: 92231894.
 RA Tsuzuki K., Kimura K., Fujii N., Yokosawa N., Oyama K.;
 RT "The complete nucleotide sequence of the gene coding for the
 RT nontoxic-nonhemagglutinin component of Clostridium botulinum type C
 RT progenitor toxin";
 RL Biochem. Biophys. Res. Commun. 183:1273-1279(1992).
 CC -1- FUNCTION: THE NONTOXIC COMPONENT IS NECESSARY TO MAINTAIN
 CC TOXICITY.
 CC -----
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 CC -----
 DR EMBL: X62389; CAA44262.1;
 DR INTERPRO: IPR000395;
 DR PRAM: PF01742; Peptidase M27; 1.
 DR PRINTS: PR00760; BONTXILIXSIN.
 KW Neurotoxin.
 SQ SEQUENCE 1196 AA; 138740 MW; 4BD5956274D7F9C3 CRC64;

Query Match 9.78; Score 78; DB 1; Length 1196;
 Best Local Similarity 24.38; Pred. No. 18;
 Matches 35; Conservative 23; Mismatches 58; Indels 28; Gaps 4;
 QY 35 IDQASEPQRLIIVYKDEVRGLAV--TLVYKSKXSTLSCNKKIISFEEMPEN-- 90
 DB 965 ISISVDRLKQDLIFL-NKKNVANSIDQLISYSINIISLVNKNNSIYVEELSVLDNPI 1023
 QY 91 -----IDDIOSDLIFQKRVPGHNKMEFESSLYEGHFLACQKEDDAFK 133
 DB 1024 TSEVIRNFYSYLDNSYIRDSSKSLLEYKNKYQLYNVPETSLYE-----VNDNKSQY 1077
 QY 134 LILKKDENGDSVWFTLNLOS 157
 DB 1078 LSLKNTDGINISSVKKFLINIDES 1101

RESULT 12
 UE3A_MOUSE
 ID UE3A_MOUSE STANDARD; PRT; 885 AA.
 AC 008759; P97482;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-
 DE ASSOCIATED PROTEIN E6-AP).
 GN UBE3A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6 X CBA;
 RX MEDLINE: 97326076.
 RA Hatakeyama S., Jensen J.P., Weissman A.M.;

RT "Subcellular localization and ubiquitin-conjugating enzyme (E2)
 RT interactions of mammalian HECT family ubiquitin protein ligases."
 RL J. Biol. Chem. 272:15085-15092(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MCDLINE: 97264343.
 RA Sutcliffe J.S., Jiang Y.-H., Galjaard R.-J., Matsura T., Fang P.,
 RA Kubota T., Christian S.L., Bressler J., Cattnach B., Ledbetter D.H.,
 RA Beaudet A.L.;
 RT "The E6-AP ubiquitin-protein ligase (UBE3A) gene is localized within
 RT a narrow Angelman syndrome critical region."
 RL Genome Res. 7:368-377(1997).
 CC -1- FUNCTION: E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM
 CC AN E2 UBIQUITIN-CONJUGATING ENZYME IN THE FORM OF A THIOESTER AND
 CC THEN DIRECTLY TRANSFERS THE UBIQUITIN TO TARGETED SUBSTRATES.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN BRAIN, HEART AND THYMUS.
 CC -1- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
 CC THIOESTER FORMATION.
 CC -1- SIMILARITY: CONTAINS 1 HECT-TYPE E3 UBIQUITIN-PROTEIN LIGASE
 CC DOMAIN.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-38 IS THE INITIATOR.
 CC -----
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 CC -----
 DR EMBL: U96636; AAB63361.1; -
 DR EMBL: U82122; AAB47756.1; -
 DR MCD: MGI105098; UBE3A.
 DR INTERPRO: IPR000569; -
 DR INTERPRO: IPR002106; -
 DR PFAM: PFO0632; HECT. 1.
 DR PROSITE: PS50237; HECT. 1.
 DR KW Nuclear protein; Ubiquitin conjugation; Ligase.
 FT DOMAIN 405 410
 FT BINDING 786 885
 FT BINDING 853 853
 FT CONFLICT 187 187
 FT CONFLICT 301 301
 FT CONFLICT 343 343
 FT CONFLICT 384 384
 FT CONFLICT 460 460
 FT CONFLICT 486 486
 FT CONFLICT 535 535
 FT CONFLICT 577 582
 FT CONFLICT 584 584
 FT CONFLICT 587 588
 FT CONFLICT 597 597
 FT CONFLICT 623 627
 FT CONFLICT 725 726
 FT CONFLICT 817 817
 FT CONFLICT 869 870
 FT SEQUENCE 885 AA; 101175 MW; 550885E080CCB699 CRC64;
 Query Match 9.5%; Score 77; DB 1; Length 885;
 Best Local Similarity 26.7%; Pred. No. 15;
 Matches 31; Conservative 20; Mismatches 35; Indels 30; Gaps 7;

QY 14 NINDOVLVDRKQPVFE--DMTIDIDASSEPOTRLIYMYKDSSEVRLAVLTVKSDSKXS 71
 DB 402 NHNEE-----DDEEIPSESELTLQELGDERRNK-----KGRVDPLETLGVK----- 446
 QY 72 TLSCNNKIISFEEM--DPENIDIOSDLIFOKRVPHNNKMEFESSLYEGHFLAC 125
 DB 447 TLDCKRLPISSEESINELNVLEMDKYTF-----KVTEN--KQSFMTG 491

RESULT 13
 ID Y809.METJA STANDARD: PRT: 167 AA.
 AC 058219;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL PROTEIN MJ0809.
 GN MJ0809.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE: 96337999.
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Utermack T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Colton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii."
 RL Science 273:1058-1073(1996).
 CC -1- SIMILARITY: BELONGS TO THE M.JANNASCHII MJ0553 / MJ0809 / MJ1331 /
 CC MJ1405 FAMILY.
 CC -----
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 CC -----
 DR EMBL: U67525; AAB98817.1; -
 DR TIGR: MJ0809; -
 DR KW Hypothetical protein.
 DR SEQUENCE 167 AA; 19723 MW; DD998FE1329C0042 CRC64;
 Query Match 9.5%; Score 76.5; DB 1; Length 167;
 Best Local Similarity 26.8%; Pred. No. 2.3;
 Matches 33; Conservative 16; Mismatches 39; Indels 35; Gaps 5;

QY 47 IIVYKDSSEVRLAVLTVKDSK-----XSTLSCNNKIISFEEMDP-----PENID 92
 DB 38 IIVYKDSSEVRLAVLTVKDSK-----XSTLSCNNKIISFEEMDP-----PENID 92
 QY 93 DIOSDLIFOKRVPHNNKMEFESSLYEGHFLACOKEDDAFLIKKKDENGKSVMTLT 152
 DB 98 RLSSDDI-----LELNKKLDEG-----VKYIKLIPAELEEH--KKVLLEIK 136
 QY 153 NLH 155
 DB 137 DMH 139
 RESULT 14
 ID HTPG_HELPY STANDARD: PRT: 621 AA.
 AC P56116;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G).
 GN HTPG OR HP0210.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;

```

OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-26695 / ATCC 700392;
RX MEDLINE; 97394467.
RA Tomb J.-F., White O., Kervavage A.R., Clayton R.A., Sutton G.C.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Colton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
CC -!- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
CC -!- SIMILARITY:
CC -----
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CC -----
DR EMBL; AE000541; AAD07278.1; -
DR HSSP; P07900; IYES.
DR TIGR; HP0210; -
DR INTERPRO; IPR001404; -
DR PFAM; PFO0183; HSP90; 1.
DR PRINTS; PR00775; HEATSHOCK90.
DR PROSITE; PS00298; HSP90; 1.
DR Chaperone; ATP-binding; Heat shock.
KW SEQUENCE 621 AA; 71274 MW; 28F198C1DC7EAB9A CRC64;
SQ
Query Match 9.5%; Score 76.5; DB 1; Length 621;
Best Local Similarity 23.2%; Pred. No. 11;
Matches 29; Conservative 27; Mismatches 52; Indels 17; Gaps 4;
OY 32 MTDIDQASEPQTRLLIYMYKDESEVRLAVTLISVK--DSKXSTLCKNKLISFEEDMP 88
DB 31 LRELVSANSPALDKLWMLTDEKLGMLNTPTSIHLSFDSQKTLIKNGIGMDNDLI 90
OY 89 ENITDI-QSDLIIFQKRVPGHNK-----EFSSLYEGHFLACQKEDDAFKLLKKDE 141
DB 91 EHLGTLAKSGTKNLFSLALSGDKRKKDSALIGQFGVGYSAFMVAS-----KIVQTKKV 143
OY 142 NGDKS 146
DB 144 NSDQA 148

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RA Revuelta J.L., Santos M.A.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; Z28315; CA882169.1; -
DR PIR; S38168; S38168.
DR SGD; S0001798; YKR090W.
DR INTERPRO; IPR001781; -
DR PFAM; PFO0412; LIM; 2.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS00423; LIM_DOMAIN_2; 2.
KW Hypothetical protein; LIM motif; Metal-binding; Zinc.
FT DOMAIN 556 612
FT DOMAIN 621 672
FT LIM
SQ SEQUENCE 706 AA; 79447 MW; B27DB9E09A39AA42 CRC64;
Query Match 9.5%; Score 76.5; DB 1; Length 706;
Best Local Similarity 22.2%; Pred. No. 13;
Matches 35; Conservative 25; Mismatches 63; Indels 35; Gaps 6;
OY 9 TAVININDQVLFVDKROVFEDMTDIDQASEPQ-----RLIYMYKDESEVRLAVTLIS 64
DB 428 TSIYONSNTNL-----SROTLVYDKGVDEDAPESTNGGPIFYFKQSNVE-----YS 478
OY 65 VKDSKXSTLSCNKLISFE--EMDPENIDDIQSDLIIFQKRVPGH----- 108
DB 479 NNEGMSQSETFRTKPLTEALQLOHKRNITDLREE--INSSNSDSHYLPNGGTRYSSDA 537
OY 109 -----NKMFEESLYEGHFLACQKEDDAFKLLKKDE 141
DB 538 DYKETPELFKYPGEGPCACGLGVTKRMFSKENE 575

```

Search completed: November 21, 2000, 23:21:41.
Job time: 322 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 21, 2000, 21:56:14 : Search time 46.58 seconds
(without alignments)
314.722 Million cell updates/sec

Title: US-09-050-249-2

Perfect score: 808
Sequence: 1 NGRRLHCTTAVIRINDVYL.....KKDENGDKSVMTLTNLS 157

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_14:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.plant:*
11: sp.potent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	522	64.6	193	09UT73	09UT73 bos taurus
2	91	11.3	987	09V718	09V718 drosophila
3	85.5	10.6	784	09Y174	09Y174 schistosoma
4	85.5	10.6	784	09Y9R6	09Y9R6 schistosoma
5	85	10.5	482	09UAI4	09UAI4 dictyosteli
6	85	10.3	483	09Y0A6	09Y0A6 dictyosteli
7	83	10.3	267	073909	073909 gallus galli
8	81	10.0	483	09XV67	09XV67 caenorhabdi
9	80.5	10.0	267	029082	029082 sus scrofa
10	80.5	10.0	414	024892	024892 elmeria max
11	80	9.9	506	084869	084869 chlamydia t
12	78.5	9.7	1039	09YF27	09YF27 aeropyrum p
13	78	9.7	388	09RF7	09RF7 streptococc
14	78	9.7	1196	045916	045916 clostridium
15	78	9.7	1196	053550	053550 clostridium
16	78	9.7	1196	038197	038197 clostridium
17	78	9.7	1196	092X77	092X77 clostridium
18	78	9.7	1247	096168	096168 plasmodium
19	77.5	9.6	366	09YVMO	09YVMO lymantilla d

20	77.5	9.6	1631	4	09Y6U6	09Y6U6 homo sapien
21	77	9.5	563	10	09SV96	09SV96 arabidopsis
22	77	9.5	672	5	09UOK1	09UOK1 plasmodium
23	76.5	9.5	905	3	094641	094641 schistosach
24	76.5	9.5	1294	10	09S814	09S814 arabidopsis
25	76	9.4	525	4	09UP58	09UP58 homo sapien
26	75.5	9.3	161	11	062161	062161 mus musculu
27	75.5	9.3	626	2	050498	050498 streptomyce
28	75.5	9.3	818	10	09SHN7	09SHN7 arabidopsis
29	75.5	9.3	866	10	024295	024295 pisum sativ
30	75	9.3	621	2	09ZM2	09ZM2 helicobacte
31	75	9.3	1146	2	051778	051778 borrelia bu
32	74.5	9.2	661	2	P73025	P73025 synechocyst
33	74.5	9.2	803	4	075283	075283 homo sapien
34	74.5	9.2	849	11	09Z283	09Z283 mus spretus
35	74.5	9.2	950	4	09UN73	09UN73 homo sapien
36	74	9.2	254	2	051029	051029 borrelia bu
37	74	9.2	445	5	09XYW4	09XYW4 drosophila
38	73.5	9.1	647	3	002892	002892 saccharomyc
39	73.5	9.1	680	3	074343	074343 schistosach
40	73.5	9.1	1128	10	09SAF6	09SAF6 arabidopsis
41	73.5	9.1	1146	2	068317	068317 vibrio chol
42	73.5	9.1	2077	12	09WT33	09WT33 human herpe
43	73.5	9.1	2077	12	09QJ37	09QJ37 human herpe
44	73	9.0	266	6	09TK1	09TK1 tursiops tr
45	73	9.0	1298	5	044199	044199 caenorhabdi

ALIGNMENTS

RESULT	1	PRELIMINARY	PRT	193 AA.
09UT73				
ID	09UT73			
AC	09UT73			
DT	01-MAY-2000 (TREMURel. 13, Created)			
DT	01-MAY-2000 (TREMURel. 13, Last sequence update)			
DT	01-MAY-2000 (TREMURel. 13, Last annotation update)			
DE	INTERLEUKIN-18 PRECURSOR.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;			
OC	Bovidae; Bovinae; Bos.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEHLIN; 20012648.			
RA	Shoda L.R., Zarling D.S., Hirano A., Brown W.C.;			
RT	"Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-			
RT	18 expression in macrophages and its IFN-gamma-inducing activity.";			
RL	J. Interferon Cytokine Res. 19:1169-1177(1999).			
DR	EMBL: AF124789; AAF08686.1; -			
SO	SEQUENCE. 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;			

Query Match 64.6%; Score 522; DB 6; Length 193;
Best Local Similarity 65.2%; Pred. No. 1.2e-40;
Matches 101; Conservative 30; Mismatches 22; Indels 2; Gaps 2;

QY	1	NGRRLHCTTAVIRINDVYLVDK-ROPVFEDMTDIQASAPOTRLIYYKSEVAGL	59
DB	37	HFGKLEKRLSIIRNLINQVLFINGNQPVEFEDMPDSDSNAPOTIRIYYKSLTGL	96
QY	60	AVTISVDSKSKSTLCKNKIISFEEMDPENIDIOSDLFFOKRVGH-NKMEFESSLY	118
DB	97	AVTISVCKKSKSTLCKNKIISFEEMDPENIDIOSDLFFOKRVGH-NKMEFESSLY	156
QY	119	EGHFLACOKEDDAFLIKKKDENGDKSVMTLTN	153
DB	157	KGYFLACKENDFLIKKKDENGDKSVMTLTN	191
RESULT	2		
QYV718			

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ID 09Y718 PRELIMINARY: PRT: 987 AA.
AC 09Y718:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CG8414 PROTEIN.
GN CG8414.
OS Drosophila melanogaster (fruit fly)
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY.
RX MEDLINE: 20196006.
RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Plamnoch C., Baldwin D.,
RA Ballev R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Gliedek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuang D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003808; AAF58067.1;
DR FLYBASE: FBgn0034073; CG8414.
SQ SEQUENCE 987 AA: 110425 MW: E10CD3B78710BCAA CRC64:

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Query Match 11.3%; Score 91; DB 5; Length 987;
Best Local Similarity 31.5%; Pred. No. 2.7;
Matches 35; Conservative 21; Mismatches 47; Indels 8; Gaps 5;
OY 24 KROP-FEEDMTDIDQASSEPOTRLITYMKDSVGRGLATVLSKDSKXSLCKNNIISF 82
DB 373 QREPLLEIFD-DPEVEKQERIEDOSVMDIYVKNLSSVPPKRESEVAITEENDEVSU 431
OY 83 EENDPENNIDIDQ-SDLIFOKRVGNHME--FESSYLEGHFLACOKED 129
DB 432 PEVVTPEKEVYLOPSPVDFY--RNQANPTELSEFENLSKNHVLAVINED 480

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ID 09Y104 PRELIMINARY: PRT: 784 AA.
AC 09Y104:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE RETINOID X RECEPTOR RXR-2.
GN RETINOID X RECEPTOR RXR-2.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NMRI.
RX MEDLINE: 99307140.
RA Freebern W.J., Niles E.G., Loverde P.T.;
RT "RXR-2, a member of the retinoid x receptor family in Schistosoma
RL mansoni."
RL Gene 233:33-38(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: AF129816; AAD33428.1;
DR INTERPRO: IPR000324;
DR INTERPRO: IPR000356;
DR INTERPRO: IPR001628;
DR PFAM: PF00104; hormone_rec. 1.
DR PFAM: PF00105; zf-C4; 1.
DR PRINTS: PR00047; STEROIDINGER.
DR PRINTS: PR00350; VITAMINDR.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger.
SQ SEQUENCE 784 AA: 87249 MW: C035E449E5F547F CRC64:

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Query Match 10.6%; Score 85.5; DB 5; Length 784;
Best Local Similarity 27.1%; Pred. No. 6.6;
Matches 32; Conservative 18; Mismatches 53; Indels 15; Gaps 4;
OY 46 LIYWKSEVGLAVITVSKKXSTLCKNKIISFEEMPPEN-IDDIOSDLIF---- 100
DB 513 LVYWLANDKPRSLSTSNSTSKLPPTTINSTDISNTDPPENSISIDSKDCTIQKK 572
OY 101 FOKRVGNHME-FESSYLEGHFLACOKEDDAFKLILKKDENGDSVYFTNLHQS 157
DB 573 IKSVPLDEKMDYYSNPERFL-----NNLTGPMNNNDSSSKPTINDN 621

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RESULT 4
ID 0909R6 PRELIMINARY: PRT: 784 AA.
AC 0909R6:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE RETINOID-X-RECEPTOR.
GN RETINOID-X-RECEPTOR.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
RN [1]
RP SEQUENCE FROM N.A.
RA Mendonca R.L., Escrivá H., Bouton D., Vanacker J.-M., Zelus D.,
RA Bonnelly E., Pierce R., Laudet V.;
RT "A Schistosoma mansoni nuclear receptor of the RXR family shows marked
RT structural and functional divergence from vertebrate and arthropod
RT homologs."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF158102; AAD45325.1;
DR INTERPRO: IPR000324;
DR INTERPRO: IPR000536;
DR INTERPRO: IPR001628;
DR INTERPRO: IPR001723;
DR PFAM: PF00104; hormone_rec. 1.
DR PFAM: PF00105; zf-C4; 1.
DR PRINTS: PR00047; STEROIDINGER.

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DR PRINTS: PR00350; VITAMINDR.
DR PRINTS: PR00398; STRDHOMOMER.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor
SO SEQUENCE 784 AA; 87250 MW; 471DAE69EB135A9F CRC64;

Query Match 10.6%; Score 85.5; DB 5; Length 784;
Best Local Similarity 27.1%; Pred. No. 6.6;
Matches 32; Conservative 18; Mismatches 53; Indels 15; Gaps 4;

QY 46 LIIVYKXSEVGLAVLTVKDKXKSLCKKKIISFEEMDPEN-IDDIOSDLIF---- 100
DB 513 LVYWLANKHKKRSLSTNSKSLPTPTPTINSTIDNPENSISDISKDTIOMKK 572
QY 101 FOKRVPGNHKE-FESSLYEGHFLACQKEDDAFKLILKKKDKNGKSVFTITNHOS 157
DB 573 INKSVPLDEKMDYYNSNPEPHLL-----NNLTKPMNNMNSDISKPTNINDN 621

RESULT 5

Q9UA14 PRELIMINARY; PRT; 482 AA.

AC Q9UA14;
DT 01-MAY-2000 (Tremblrel. 13; Created)
DT 01-MAY-2000 (Tremblrel. 13; Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14; Last annotation update)
DE PROTEIN PHOSPHATASE 2A 55 KDA REGULATOR B SUBUNIT (FRAGMENT).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Dictyostelida; Dictyostelium.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99379588.
RA Murphy M.B., Levy S.K., Egelhoff T.T.;
RT "Molecular characterization and immunolocalization of Dictyostelium
RT discoideum protein phosphatase 2A.";
RL FEBS Lett. 456:7-12(1999).
DR EMBL; AF138279; AAD29694.1; -
DR INTERPRO; IPR000009; -
DR INTERPRO; IPR001680; -
DR PFAM; PF01240; PR55; 1.
DR PRINTS; PR00600; P2APR55.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
DR PROSITE; PS01024; PR55_1; 1.
DR PROSITE; PS01025; PR55_2; 1.
FT NO_TERM 1
SO SEQUENCE 482 AA; 55107 MW; 95E879E7A37D2392 CRC64;

Query Match 10.5%; Score 85; DB 5; Length 482;
Best Local Similarity 25.9%; Pred. No. 4.2;
Matches 36; Conservative 23; Mismatches 58; Indels 22; Gaps 6;

QY 14 NINDOVL-FVKKRQVFEDMTDIDQASEPOTRLIIVYKXSEVGLAVLTVKDKXKST 72
DB 236 NINTECFNVVDIKPTNMDLLEVTISAEFHTSCNIFMYSK-----GTIKGLDRSSA 290
QY 73 LSCNKKIISFEEMDPENIDDIOSDLIFOKRVPGNHKEFESSLYEGHFLACQKEDDAF 132
DB 291 L-CDNHAVFEYEDPSKMS-----FFSELISSISDIKFSR---DGRYILSRD----- 334
QY 133 KLILKKKDKNGKSVFTL 151
DB 335 FLTLKMDINMKNKPKVTI 353

RESULT 6

Q9Y0A6 PRELIMINARY; PRT; 483 AA.

AC Q9Y0A6;
DT 01-NOV-1999 (Tremblrel. 12; Created)
DT 01-NOV-1999 (Tremblrel. 12; Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13; Last annotation update)

DE PROTEIN PHOSPHATASE 2A B55 REGULATORY SUBUNIT.
GN pppd.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Dictyostelida; Dictyostelium.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-AX4;
RA Campanha R.B., Etcheberry L.C., da Silva A.M.;
RT "Functional analysis of a B regulatory subunit of protein phosphatase
RT 2A in D. discoideum"; to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167979; AAD45396.1; -
DR INTERPRO; IPR000009; -
DR INTERPRO; IPR001680; -
DR PFAM; PF01240; PR55; 1.
DR PRINTS; PR00600; P2APR55.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
DR PROSITE; PS01024; PR55_1; 1.
DR PROSITE; PS01025; PR55_2; 1.
SO SEQUENCE 483 AA; 55375 MW; DCF9434FE95C27BE CRC64;

Query Match 10.5%; Score 85; DB 5; Length 483;
Best Local Similarity 25.9%; Pred. No. 4.2;
Matches 36; Conservative 23; Mismatches 58; Indels 22; Gaps 6;

QY 14 NINDOVL-FVKKRQVFEDMTDIDQASEPOTRLIIVYKXSEVGLAVLTVKDKXKST 72
DB 237 NINTECFNVVDIKPTNMDLLEVTISAEFHTSCNIFMYSK-----GTIKGLDRSSA 291
QY 73 LSCNKKIISFEEMDPENIDDIOSDLIFOKRVPGNHKEFESSLYEGHFLACQKEDDAF 132
DB 292 L-CDNHAVFEYEDPSKMS-----FFSELISSISDIKFSR---DGRYILSRD----- 335
QY 133 KLILKKKDKNGKSVFTL 151
DB 336 FLTLKMDINMKNKPKVTI 354

RESULT 7

ID 073909 PRELIMINARY; PRT; 267 AA.

AC 073909;
DT 01-AUG-1998 (Tremblrel. 07; Created)
DT 01-AUG-1998 (Tremblrel. 07; Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13; Last annotation update)
DE INTERLEUKIN-1BETA.
GN IL-1BETA.
OS Gallus gallus (Chicken).
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RA Weinig K.C., Sick C., Kaspers B., Staeheli P.;
RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y15006; CA75239.1; -
DR HSSP; P18510; IIRA.
DR INTERPRO; IPR000975; -
DR PFAM; PF00340; Interleukin-1; 1.
DR PROSITE; PS00253; INTERLEUKIN-1; 1.
FT CHAIN 106 267 INTERLEUKIN-1BETA.
SO SEQUENCE 267 AA; 29822 MW; 3EF72164E4D40B64 CRC64;

Query Match 10.3%; Score 83; DB 13; Length 267;
Best Local Similarity 24.8%; Pred. No. 3.2;
Matches 30; Conservative 18; Mismatches 45; Indels 28; Gaps 4;

QY 31 DMTDIDQ-----ASEPOTRLIIVYKXSEVGLA-----VTLISVK 66
DB 118 DIFDINGCFVLESPTQVALVHLQGPSSSQKVRNLIALYRGRPGSGAGTQMPVALGIK 177

QY 67 DSK---XSTLCKNKKIISFEEMDPDENIDIO-SDLIFFOKRVPGHNMKEFESSLYEGHF 122
 DB 178 GYKLYMNCVMSGTEPTQLLEADYMDRODSVELTRIFIFRLDSTEGTTRFESAAPFGWF 237
 QY 123 L 123
 DB 238 I 238

RESULT 8
 ID Q9XV67 PRELIMINARY; PRT: 483 AA.
 AC Q9XV67
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE F25C8.2 PROTEIN.
 GN F25C8.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 NC Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA Matthews L.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans";
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 Lightning J., Lloyd C., Murray A., Mortimore B., O'Callaghan M.,
 Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 Smealon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
 Watson A., Wellstock L., Wilkinson-Sproat J., Wollman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans";
 RL Nature 368:32-38(1994).
 DR EMBL: Z81512; CAB04171.1;
 DR INTERPRO: IPR002937;
 DR PFAM: PF01593; Amino-oxidase; 1.
 SO SEQUENCE 483 AA; 55505 MW; 172CEC91495557AB CRC64;

Query Match 10.0%; Score 81; DB 5; Length 483;
 Best Local Similarity 26.4%; Pred. No. 9.8; Mismatches 63; Indels 66; Gaps 12;
 Matches 55; Conservative 24;

QY 3 GRLHCTAVIRINDQY-----LFVDRQPVFEDMTDIDOSAS-----EPQIFLI 48
 DB 81 GYLHFGAEYVNGVDENVNLVEKYDLF-DKTPTDMLMDQDNSTIYNGLHVPKIL 139
 QY 49 YMKDSVRLAVLTSKXSKSTLSCKNKIIS-FEEM--DPPENIDIOSDLIFFOKRV 105
 DB 140 DKFND-YIRLVNALVEKSIKINOLSVENINNOFIFELADVENDAEIYESLIYVK 196
 QY 106 PGHNMKEFESSLYEGHFL-----ACQKEDDA-----FKLIK----- 137
 DB 197 ---NYFOTEMSSPYGEISLNSLISWDGTDEEDSAVLNKGQFEIILDFRSKIPAGNIRL 253
 QY 138 -----KDGNDKSVYFTLTN---LH 155
 DB 254 NCEVINVKEEN-----IMVLKNGEYVH 277

ID 029082. PRELIMINARY; PRT: 267 AA.
 AC 029082;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE INTERLEUKIN 1-BETA.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Vanderbroeck K.;
 RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE: 94039070.
 RA Vanderbroeck K., Fiten P., Beuken E., Martens E., Janssen A.,
 Van Damme J., Opdenacker G., Billiau A.;
 RT "Gene sequence, cDNA construction, expression in Escherichia coli and
 genetically approached purification of porcine interleukin-1 beta.";
 RL Eur. J. Biochem. 217:45-52(1993).
 DR EMBL: X74568; CAA52660.1;
 DR HSSP: P01584; 1H1B.
 DR INTERPRO: IPR000975;
 DR INTERPRO: IPR002348;
 DR PFAM: PF00340; Interleukin-1; 1.
 DR PRINTS: PR00262; IL1HGF.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 SO SEQUENCE 267 AA; 29893 MW; 4830645DA5FF9967 CRC64;

Query Match 10.0%; Score 80.5; DB 6; Length 267;
 Best Local Similarity 28.6%; Pred. No. 5.5; Mismatches 25; Indels 13; Gaps 6;
 Matches 24; Conservative 22;

QY 53 DSEVRLAVLTSKXSKSTLSCKNK---IISFEEMDP---PENIDIOSDLIFFOKRV 105
 DB 165 DSDKD-IPYTLGK-GKNLYLSCVMKDDPTQLLEADVDPKSYPKR--DMKRFVFKTEI 220
 QY 106 PGHNMKEFESSLYEGHFLACQKED 129
 DB 221 --KNRYEFESALYPMYISTSQAE 242

RESULT 10
 ID 024892 PRELIMINARY; PRT: 414 AA.
 AC 024892;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE CALMODULIN-DOMAIN PROTEIN KINASE (FRAGMENT).
 OS Eimeria maxima.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
 NC Eimeria.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HOUGHTON;
 RX MEDLINE: 96089387.
 RA Bumstead J.M., Dunn P.P.J., Tomley F.M.;
 RT "Nitrocellulose immunoblotting for identification and molecular gene
 cloning of Eimeria maxima antigens that stimulate lymphocyte
 proliferation.";
 RL Clin. Diagn. Lab. Immunol. 2:524-530(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HOUGHTON;
 RX MEDLINE: 97048698.
 RA Dunn P.P.J., Bumstead J.M., Tomley F.M.;
 RT "Sequence, expression and localization of calmodulin-domain protein

SO SEQUENCE 388 AA: 42720 MW: 90766A76805BCE45 CRC64:

Query Match 9.7%; Score 78; DB 2; Length 388;

Best Local Similarity 20.1%; Pred. No. 14; Matches 27; Conservative 25; Mismatches 70; Indels 12; Gaps 3;

OY 28 VEDMTDIDQASBPOTRLIITYWKDSEVRGLAVILSVKDSKXSTLSCNKKIISFEEMP 87

DB 169 VYKYVDPSOCPKNGKVMGLGFTDPTGVFASAVTGOVEEDTSLFTKNEFTFYDENQ 228

OY 88 PENIDIOISDLIFFOKRVPGHKNMEFESSLYEGHFLACQED-----DAFKLILKKK 139

DB 229 PTFDALLSVASLNE---HNSIEMAKD-YSGTFIKIGSSIGENGMIVATKTLNFRK 284

OY 140 DENGKDSVMEFTLTN 153

DB 285 DOGGSRTMYPRAN 298

RESULT 14

ID 045916 PRELIMINARY: PRT: 1196 AA.

AC 045916: 01-NOV-1996 (Tremblrel. 01, Created)

DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)

DE 01-UN-2000 (Tremblrel. 14, Last annotation update)

GN 138 KDA PROTEIN ASSOCIATED WITH BONT /C1-HAEMAGGLUTININ COMPLEX.

OS Clostridium botulinum.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;

CC Clostridium.

RP SEQUENCE FROM N.A. Popoff M.R.;

RA Hauser D.F., Eklund M.W., Popoff M.R.;

RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.

DR EMBL: X66433; CAA47059.1; -

DR INTERPRO: IPR000395; -

DR PFAM: PF01742; Peptidase_M27; 1

DR PRINTS: PR00760; BONTOTOXITIN.

DR PRODOM: PD001963; -; 1

SO SEQUENCE 1196 AA: 138725 MW: 88D5956301FA4A91 CRC64;

Query Match 9.7%; Score 78; DB 2; Length 1196;

Best Local Similarity 24.3%; Pred. No. 53; Matches 35; Conservative 23; Mismatches 58; Indels 28; Gaps 4;

OY 35 IDQASEPOTRLIITYWKDSEVRGLAV--TLVYKDSKXSTLSCNKKIISFEEMPEN-- 90

DB 965 ISISVDRKQDLIFT-NDKNVANVSIDQILSTIYSTINISLVKNKNSIYVELSVLDNPI 1023

OY 91 -----IDDIQSDLIFFOKRVPGHKNMEFESSLYEGHFLACQEDDAFK 133

DB 1024 TSEEVIRNYFSYLDNSYIRDSKSLLEYKNKYOLYNYVFPETSLYE-----VNDNKKSY 1077

OY 134 LILKKDENGKDSVMEFTLTNLOS 157

DB 1078 LSLKNTDGINISSVKEKLINIDES 1101

RESULT 15

ID 053550 PRELIMINARY: PRT: 1196 AA.

AC 053550: 01-NOV-1996 (Tremblrel. 01, Created)

DT 01-NOV-1996 (Tremblrel. 13, Last sequence update)

DE PROGENITOR TOXIN L NONTOTOXIC-NONHEMAGGLUTININ COMPONENT (FRAGMENT).

OS Clostridium botulinum.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;

CC Clostridium.

RP SEQUENCE FROM N.A. MEDLINE: 96025415.

RA Ohyama T., Watanabe T., Fujinaga Y., Inoue K., Sunagawa H., Fujii N.,

RA Inoue K., Oguma K.,

RT "Characterization of nontoxic-nonhemagglutinin component of the two

RT types of progenitor toxin (M and L) produced by Clostridium botulinum

RT type D CB-16."

RL Microbiol. Immunol. 39:457-465(1995).

DR EMBL: S80809; AAB36016.2; -

DR INTERPRO: IPR000395; -

DR PFAM: PF01742; Peptidase_M27; 1.

FT NON_TER 1196 1196

SO SEQUENCE 1196 AA: 138717 MW: 6D2DB5F6AF38324 CRC64;

Query Match 9.7%; Score 78; DB 2; Length 1196;

Best Local Similarity 24.3%; Pred. No. 53; Matches 35; Conservative 23; Mismatches 58; Indels 28; Gaps 4;

OY 35 IDQASEPOTRLIITYWKDSEVRGLAV--TLVYKDSKXSTLSCNKKIISFEEMPEN-- 90

DB 965 ISISVDRKQDLIFT-NDKNVANVSIDQILSTIYSTINISLVKNKNSIYVELSVLDNPI 1023

OY 91 -----IDDIQSDLIFFOKRVPGHKNMEFESSLYEGHFLACQEDDAFK 133

DB 1024 TSEEVIRNYFSYLDNSYIRDSKSLLEYKNKYOLYNYVFPETSLYE-----VNDNKKSY 1077

OY 134 LILKKDENGKDSVMEFTLTNLOS 157

DB 1078 LSLKNTDGINISSVKEKLINIDES 1101

Search completed: November 21, 2000, 23:20:57

Job time: 5083 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2000, 17:23:54 ; Search time 71.63 seconds

(without alignments)
2470.154 Million cell updates/sec

Title: US-09-050-249-1

Perfect score: 471
Sequence: 1 AACTTGGCCGACCTCACTG.....TCACCTACTCATCAAGT 471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

N.Geneseq_36:*

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- 5: /cgn2_2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
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- 20: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
- 21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470.6	99.9	471	17 T32403	Mouse interferon-g
2	470.6	99.9	471	17 T16224	Interferon gamma p
3	470.6	99.9	471	18 T60536	Mouse interferon-g
4	470.6	99.9	471	18 T80210	Murine protein for
5	470.6	99.9	471	19 V48227	Mouse interleukin
6	470.6	99.9	471	21 Z35923	DNA encoding a pro
7	470.6	99.9	570	19 V32755	Wild-type mouse in
8	469	98.6	471	19 V32633	Mutant mouse inter
9	467.4	99.2	471	19 V32632	Mutant mouse inter
10	400.6	85.1	722	19 V20875	Nucleotide sequenc
11	279.8	59.4	665	19 V20876	Nucleotide sequenc
12	268.4	57.0	582	21 Z55624	Equine interleukin

13	249.2	52.9	477	21 A10526	Human interleukin-
14	247.8	52.6	471	19 V48226	Human interleukin
15	247.8	52.6	471	19 V32625	Mutant human inter
16	247.8	52.6	471	19 V32626	Mutant human inter
17	247.8	52.6	570	19 V32754	Wild-type human in
18	247.8	52.6	1101	18 T74988	Interferon gamma 1
19	247.8	52.6	1101	18 T74987	Interferon gamma 1
20	247.8	52.6	1380	19 V05368	CDNA encoding huma
21	247.4	52.5	471	17 T32411	Human interferon-g
22	247.4	52.5	471	17 T32412	Human interferon-g
23	247.4	52.5	471	18 T80209	Human protein for
24	247.4	52.5	471	21 Z36875	DNA encoding a mat
25	247.4	52.5	579	19 V18906	Interferon-gamma 1
26	247.4	52.5	579	19 V17200	Interferon-gamma 1
27	247.4	52.5	1120	17 T32404	Human interferon-g
28	247.4	52.5	1120	19 V18825	CDNA for interfero
29	247.4	52.5	1120	21 Z36876	DNA encoding a pro
30	246.2	52.3	471	19 V33627	Mutant human inter
31	246.2	52.3	471	19 V33628	Mutant human inter
32	244.6	51.9	471	19 V48229	Human interleukin
33	244.6	51.9	471	19 V32629	Mutant human inter
34	244.6	51.9	471	19 V32630	Mutant human inter
35	244.4	51.9	540	20 X27732	Recombinant canine
36	244.4	51.9	540	21 A13801	Canine interleukin
37	244.4	51.9	582	20 X27724	Canine interleukin
38	244.4	51.9	582	21 A13793	Canine interleukin
39	244.4	51.9	582	21 Z55623	Canine interleukin
40	244.4	51.9	1427	20 X27726	Canine interleukin
41	244.4	51.9	1427	21 A13795	Canine interleukin
42	243	51.6	471	19 V48230	Human interleukin
43	243	51.6	471	19 V32631	Mutant human inter
44	127.8	27.1	11464	19 V48228	Interleukin 18 con
45	127.8	27.1	28994	19 V15826	Genomic DNA for in

ALIGNMENTS

RESULT	1	
T32403		
ID	T32403 standard; CDNA to mRNA; 471 BP.	
XX		
AC	T32403;	
XX		
DT	29-SEP-1996 (first entry)	
XX		
DE	Mouse interferon-gamma inducer protein CDNA.	
XX		
XX	Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;	
KW	antitumour; antibacterial; immunoregulatory; adoptive immunotherapy;	
KW	therapy; cancer; ds.	
XX		
OS	Mus sp.	
XX		
PN	EP12931-A2	
XX		
PD	22-MAY-1996	
XX		
PE	10-NOV-1995; 95EP-0308055.	
XX		
PR	29-SEP-1995; 95JP-0274988.	
PR	15-NOV-1994; 94JP-0304203.	
PR	23-FEB-1995; 95JP-0058240.	
PR	10-MAR-1995; 95JP-0078357.	
PR	18-SEP-1995; 95JP-0262062.	
XX		
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.	
XX		
PI	Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;	
PI	Taniguchi M, Tanimoto T, Torigoe K, Ushio S,	
DR	WPI; 1996-252837/26.	
DR	P-PDB; R99559.	

XX DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
 PT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders

PS Example A-3-2: Page 36-37; 48pp; English.

XX A cDNA clone (T32403) codes for a novel mouse protein (R99559) that
 CC induces interferon-gamma (IFN-gamma) prodn. by immunocompetent cells.
 CC The clone was obtained from a mouse liver cDNA library by PCR
 CC amplification using primers (see also T32405-06) based on tryptic
 CC peptides (R99561-62) of the protein. A DNA fragment based on
 CC the cDNA clone was used to screen a human liver cDNA library,
 CC leading to the isolation of a clone (T32402) coding for human mature
 CC IFN-gamma inducer protein (R99558), a useful therapeutic agent.

XX Sequence 471 BP; 162 A; 91 C; 92 G; 125 T; 1 other;

Query Match 99.9%; Score 470.6; DB 17; Length 471;
 Best Local Similarity 100.0%; Pred. No. 5.8e-124;
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 1 AACTTGGCCGACTTCTACGTATACACCGAGTAATATTAATGACCAAGTTCTC 60
 DB 1 aactttggccgacttctacgtatatacaccgagtaataatgacccaagttctc 60
 YY 61 TTCGTTGACAAAAGACAGCCTGTGTTGAGAGATATGACTGATATTAATGACCAAGT 120
 DB 61 ttctgtgacaaaagacagcctgtgttcgagagatattgactgatatgatacaagtgccagt 120
 YY 121 GAACCCAGACCGAGTAT 180
 DB 121 gaacccagacccgagtagataataataatgatacaagagagagaaagagagagagagag 180
 YY 181 GTGACCCCTCTGTGAGAGATAGTAATAAAGTCTACCCCTCTCTGTAGAGAACAAAGATCATT 240
 DB 181 gtgacccctctgtgagagatagtaataaagtgctacccctctctgtagagaaagagatcatt 240
 YY 241 TCCTTTGAGAAATGATGATCCACCTGAATAATATGATGATATATATATATATATATAT 300
 DB 241 tcctttgagaaatgattgacccctgaataatattgattgataataaagtgatccatttc 300
 YY 301 TTTCAGAAAGCTGTTCAGAGACACACAAAGATGAGATTGATATCTTACATGATGAGGA 360
 DB 301 ttccagaaagctgttcagagacacacaaagatgagattgataatcttcacagtgatgagga 360
 YY 361 CACTTCTTGCTTGCACAAAAGAGATGATGCTTTCAAACTCATTTGAAAAAAGAGAT 420
 DB 361 cacttcttgcttgcacaaaagagatgattgctttcaaaactcatcttcaaaaagagat 420
 YY 421 GAAAAATGGGATTAATCTGTAATGTTTACTCTCTACTACTACTACTACTACTACTACT 471
 DB 421 gaaaatgggataatctgtatgatttactctctactactactactactactactactact 471

RESULT 2

ID T16224 standard: cDNA to mRNA; 471 BP.

AC T16224;

DT 02-SEP-1996 (first entry)

DE Interferon gamma production inducer protein coding sequence.

XX Interferon gamma; inducer; IFN-gamma; immunocompetent cell; antiviral;
 KW antitumor; antiseptic; immunoregulatory; platelet-increasing agent;
 KW therapy; prevention; condyloma acuminatum; renal cancer; brain cancer;
 KW granuloma; mycosis fungoides; rheumatism; allergy; cytotoxicity; AIDS;
 KW killer T-cell; interleukin-2; IL-2; tumor necrosis factor; TNF;
 KW adoptive immunotherapy; monoclonal antibody; ds.

OS Mus musculus.

XX EF692536-A2.

XX 17-JAN-1996.

PF 13-JUL-1995; 95EP-0304906.

XX 10-FEB-1995; 95JP-0045057.

PR 14-JUL-1994; 94JP-0184162.

XX (HAYB) HAYASHIBARA SEIBUTSU KAKAKU.

PI Kohno K, Kunikata T, Kurimoto M, Okamura H, Taniguchi M.

PI Tanimoto T, Torigoe K;

DR WPI: 1996-070177/08.

DR P-PSDB; R92506.

PS Claim 4; Page 22-23; 30pp; English.

This sequence represents the coding sequence for the interferon gamma (IFN-gamma) inducer protein of the invention. The encoded protein induces IFN-gamma production in immunocompetent cells. The protein is useful as an antiviral, antitumor, antiseptic, immunoregulatory and platelet-increasing agent. It can be used for treating or preventing AIDS, condyloma acuminatum, renal or brain cancer, granuloma, mycosis fungoides, rheumatism and allergy. The protein can also be used to induce IFN-gamma production in cultured cells. The IFN-gamma inducer strongly induces cytotoxicity of killer T-cells and when used with interleukin-2 (IL-2) and tumor necrosis factor (TNF), may improve the effect (or reduce side effects) of adoptive immunotherapy in tumors. This sequence can be used to produce the protein, which can then be purified (or assayed) using monoclonal antibodies.

SO Sequence 471 BP; 162 A; 91 C; 92 G; 125 T; 1 other;

Query Match 99.9%; Score 470.6; DB 17; Length 471;
 Best Local Similarity 100.0%; Pred. No. 5.8e-124;
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 1 AACTTGGCCGACTTCTACGTATACACCGAGTAATATTAATGACCAAGTTCTC 60
 DB 1 aactttggccgacttctacgtatatacaccgagtaataatgacccaagttctc 60
 YY 61 TTCGTTGACAAAAGACAGCCTGTGTTGAGAGATATGACTGATATTAATGACCAAGTCCAGT 120
 DB 61 ttctgtgacaaaagacagcctgtgttcgagagatattgactgatatgatacaagtgccagt 120
 YY 121 GAACCCAGACCGAGTAT 180
 DB 121 gaacccagacccgagtagataataataatgatacaagagagagagagagagagagagag 180
 YY 181 GTGACCCCTCTGTGAGAGATAGTAATAAAGTCTACCCCTCTCTGTAGAGAACAAAGATCATT 240
 DB 181 gtgacccctctgtgagagatagtaataaagtgctacccctctctgtagagaaagagatcatt 240
 YY 241 TCCTTTGAGAAATGATGATCCACCTGAATAATATGATGATATATATATATATATATATAT 300
 DB 241 tcctttgagaaatgattgacccctgaataatattgattgataataaagtgatccatttc 300
 YY 301 TTTCAGAAAGCTGTTCAGAGACACACAAAGATGAGATTGATATCTTACATGATGAGGA 360
 DB 301 ttccagaaagctgttcagagacacacaaagatgagattgataatcttcacagtgatgagga 360
 YY 361 CACTTCTTGCTTGCACAAAAGAGATGATGCTTTCAAACTCATTTGAAAAAAGAGAT 420
 DB 361 cacttcttgcttgcacaaaagagatgattgctttcaaaactcatcttcaaaaagagat 420

[illegible]

DT 13-MAR-2000 (first entry)

OY		61	TTCGTTGCACAAAGACAGCCTGGTTCGAGGATGATGACTGATGTGATCAAGAATGCCAGT	120
Dd		61	tctgttgacaaaagaacaagcctggttccgaggatatagactcgatatgcatacaagtcacgt	120
OY		121	GAAOCCCGACACAGACTGATATATATACATGTACAAGACAGTGGAAGTAAGAGACTGGCT	180
Dd		121	gaoccccagaccagactgataatacatatcatacgtacaagaacagtgaagtaagaagactggct	180
OY		181	GTGACCCTCTCTGTAAGGATATATAAAGTCTACCCCTCCTGTGAAGAACAGATCATT	240
Dd		181	gtgaccctctctgtgaaggatagaataaaygtcacccctctctgtlaagaacaagaatcatc	240
OY		241	TCCCTTTGAGGAATGAGTCCACCTGAAAATATTGATGATATACAAAGTAGTCTCATATTC	300
Dd		241	tccctttgaggaaatgatcatccactgtaaatattgatgatatacaagaagtcatcatc	300
OY		301	TTTCAGAAACGTGTTCCAGACACCAACAAGATGAGGATTGAATCTTCCACTGTATGAAGA	360
Dd		301	tttcagaaacgvtgtccagagcacacaagaatgtaggtttgaaatcttcactgtatgaagga	360
OY		361	CACCTTGTGCTTGCCAAAAAGAGATGATGCTTCAACACTATCTGAAAAAAGAGT	420
Dd		361	caccttgcvtcttgccaagaagaagatgagcttcaaactcatctcgaaaaaaggat	420
OY		421	GAANAATGGGATAAATCTGTAAATGTTCACTCTCACTAACCTACATCAANAGT	471
Dd		421	gaaatgggataaatactgtaaatgttcaactctcacctaactcatcaaaagt	471
RESULT		7		
V32755	ID	V32755	standard; cDNA; 570 bp.	
XX	AC	V32755;		
XX	DT	25-SEP-1998	(first entry)	
DE	XX	Wild-type mouse interferon-gamma inducing factor cDNA.		
KW	Interferon-gamma inducing factor; interferon-gamma; killer cell;			
KM	antitumour agent; antiviral agent; antimicrobial agent; tumour; mGIF			
KW	hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;			
KM	osteoporosis; thrombopenia; acquired immunodeficiency syndrome; ds.			
XX	Mus sp.			
OS				
XX				
FH	key	Location/Qualifiers		
FT	5'UTR	1..15		
FT		/*tag= a		
FT	CDS	16..558		
FT		/*tag= b		
FT		/product= "Immature mouse iGIF"		
FT	sig-peptide	16..84		
FT		/*tag= c		
FT		/note= "this sequence claimed by the inventors		
FT	mat_peptide	85..555		
FT		/*tag= d		
FT	3'UTR	559..570		
FT		/*tag= e		
XX				
PN	EP845530-A2.			
XX				
PD	03-JUN-1998.			
XX				
PF	28-NOV-1997;	97EP-0309632.		
XX				
PR	14-NOV-1997;	97JP-0329715.		
PR	29-NOV-1996;	96JP-0330307.		
PR	21-JAN-1997;	97JP-0020906.		
PA	(HAYB) HAYSHIBARA SEIBUTSU KAKAKU.			

```

XX Kurimoto M, Okamoto I, Yamamoto K;
PI WPI: 1998-288747/26.
DR P-PSDB: W48960.
XX Mutants of interferon-gamma inducing polypeptide - useful as
PT antitumour, antiviral, antimicrobial or anti-immunopathic agents
XX Claim 11; pages 38-39; 59pp; English.
XX
XX The present sequence represents the wild-type mouse interferon-gamma
XX inducing factor (mIGIF) cDNA. The invention provides for mutant mouse
XX and human interferon-gamma inducing factors in which one or more
XX cysteine residues are replaced with different residues at or away from
XX the consensus sequences shown in W48956-W48958. The mutant mIGIFs are
XX capable of stimulating immunocompetent cells for the production of
XX interferon-gamma and are claimed to be less toxic, more active and
XX stable than the corresponding wild type interferon-gamma inducing
XX factor. The mutant mIGIFs are also claimed to enhance killer cell
XX cytotoxicity and/or induce killer cell formation, and may therefore
XX be useful as antitumour agents, antitumour immunotherapeutics, antiviral
XX agents and antimicrobial agents. The mutant mIGIFs are also claimed
XX to be useful for treating hepatitis, acquired immunodeficiency syndrome
XX (AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal
XX carcinoma), rheumatism, osteoporosis and thrombopenia caused by
XX radiation- and chemo-therapy.
XX
XX Sequence 570 BP; 175 A; 123 C; 121 G; 151 T; 0 other;
XX
Query Match          99.9%; Score 470.6; DB 19; Length 570;
Best Local Similarity 99.8%; Pred. No. 6,2e-124;
Matches 470; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AACTTTGGCCGACTTACAGCCGAGTATACGAAATTAATGACCAAGTTCTC 60
DB 85 aactttggccgacttaccgtacacacccgcatatccgaataataatgaccaagttctc 144
XX
QY 61 TTGGTTGACAAAGACAGCCTGTGTGGAGATATGATGATTTATCAAGTGGCAAT 120
DB 145 ttggttgacaaagacagcctgtgtggagatattgatatgataaagtggcaagt 204
XX
QY 121 GAACCCGACACGACGATATATATATATATACAAAGAGTAGAGAGAGTGGCT 180
DB 205 gaacccgacacgacgacgataataatatacacaagcagtgaaagtagagagctggct 264
XX
QY 181 GTGACCTCTCTGTGAGAGATAGTAATAGTACCCTCTCTGTAGAGAACAGATCAIT 240
DB 265 gtgacctctctgtgagagatagtaaatgttaccctctcctgtgaagaacaagatcatt 324
XX
QY 241 TCGTTTGAGAAATGATCCACCTCGAAATATATGATATACAAATGATCATATTC 300
DB 325 tcccttgagaaatgataccaccctgaaataattgatatatacaaaagtgtccataatc 384
XX
QY 301 TTTCAGAACTGTTCAGACACACAAAGATGAGATTGATCTTCACTGTATGAAGA 360
DB 385 ttccagaaactgttccagacacacaaagatgagattgatacttcactgtatgaagga 444
XX
QY 361 CACTTTCTTGTGCGCAAGAGAGATGATCTTCAACATCATTTGAAAAAAGAGAT 420
DB 445 cacttctctgtgcgcaaaagagatgatgtcttcaacatcttcgaaaaaagagat 504
XX
QY 421 GAAATGGGGAATATCTGTATGTTCTACTCTACTACTACTACTACTACTCAAGT 471
DB 505 gaaatggggaaatattctgtatgttctactctactactactactactcaagaagt 555
XX
RESULT 8
ID V32633 standard; cDNA; 471 BP.
XX V32633;
AC V32633;

```

```

XX 25-SEP-1998 (first entry)
XX
XX Mutant mouse, interferon-gamma inducing factor cDNA mIGIF/MUT12.
DE
XX Interferon-gamma inducing factor; interferon-gamma; killer cell;
XX antitumour agent; antiviral agent; antimicrobial agent; tumour; mIGIF;
XX hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
XX osteoporosis; thrombopenia; acquired immunodeficiency syndrome; ds.
XX
XX Mus sp.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 1..471
XX /tag= a
XX /product= "Mutant human interferon-gamma inducing
XX factor mIGIF/MUT12."
XX /note= "CDS does not contain a stop codon"
XX mutation 373..375
XX /tag= b
XX /note= "Changed from TGC in wild-type to AGC in
XX mutant"
XX
XX EP845530-A2.
XX
XX 03-JUN-1998.
XX
XX 28-NOV-1997; 97EP-0309632.
XX
XX 14-NOV-1997; 97JP-0329715.
XX 29-NOV-1996; 96JP-0333037.
XX 21-JAN-1997; 97JP-0020906.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Kurimoto M, Okamoto I, Yamamoto K;
XX
XX WPI: 1998-288747/26.
XX P-PSDB: W48969.
XX
XX Mutants of interferon-gamma inducing polypeptide - useful as
XX antitumour, antiviral, antimicrobial or anti-immunopathic agents
XX
XX Claim 10; page 50; 59pp; English.
XX
XX The present sequence represents the mutant mouse interferon-gamma
XX inducing factor cDNA mIGIF/MUT12. The wild-type mouse, interferon-gamma
XX factor (mIGIF) cDNA sequence is shown in V32755. The invention provides
XX for mutant human and mouse interferon-gamma inducing factors in which one
XX or more cysteine residues are replaced with different residues at or away
XX from the consensus sequences shown in W48956-W48958. The mutant mIGIFs
XX are capable of stimulating immunocompetent cells for the production of
XX interferon-gamma and are claimed to be less toxic, more active and
XX stable than the corresponding wild type mIGIF factor. The mutant mIGIFs
XX are also claimed to enhance killer cell cytotoxicity and/or induce killer
XX cell formation, and may therefore be useful as antitumour agents,
XX antitumour immunotherapeutics, antiviral agents and antimicrobial agents.
XX The mutant mIGIFs are also claimed to be useful for treating hepatitis,
XX acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid
XX malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
XX thrombopenia caused by radiation- and chemo-therapy.
XX
XX Sequence 471 BP; 163 A; 91 C; 92 G; 125 T; 0 other;
XX
Query Match          99.6%; Score 469; DB 19; Length 471;
Best Local Similarity 99.6%; Pred. No. 1.6e-123;
Matches 469; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 AACTTTGGCCGACTTACAGCCGAGTATACGAAATTAATGACCAAGTTCTC 60
DB 1 aactttggccgacttaccgtacacacccgcatatccgaataataatgaccaagttctc 60

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Db 170 tctgtgacaaagaaacccgctgtgtcaggacatgcctatcgcgcgaacagcca 229
Oy 119 GTGAACCCAGACGACGATATATACATGTACAAAAGACAGTGAAGAACAGACGTCG 178
Db 230 acgaatcccaagccagcagcagataatataatgacaaagataagtaagaagagcgtg 289
Oy 179 CTGTGACCCCTCTCTGTGAAGATAGTAAAYGCTACCTCTCTGTAGAACAGATCA 238
Db 290 cgtgacccctactcgtgagagatgtaagaagtgtctaccctcccgtaaaacaaatca 349
Oy 239 TTTCTTTGAGGAATGATCCACCTGAAATATTGATATATACAAAGTATCTCATAT 298
Db 350 tttcctctt----- 358
Oy 299 TCTTTCAGAAAGCTGTTCAGGACACAAACAGATGAGTGTGATCTTCTGATGANG 358
Db 359 -----agaaacgtgtcgcagacacacaaatgaaattgaaattcctcgtatgaag 412
Oy 359 GACACTTCTGCTGCTGCCAAAGAAAGATGATGCTTCAACTCTGAAAAAAGG 418
Db 413 gcaactttctagcttgcacaaagagatgatgcttcaactcgttttgaagaaagag 472
Oy 419 ATGAAATGCGGATTAATCTGTAATGTTCTACTCTCACTACCTTACATCAAGT 471
Db 473 atgaataatgggataaatctgtcaatcgtcacttactactacatcaagaat 525
```

RESULT 12

255624 standard; cDNA; 582 BP.

255624;

27-MAR-2000 (first entry)

Equine Interleukin-18 (IL-18) cDNA.

Interleukin-18; IL-18; adjuvant; vaccine; immune reaction; equine; ss.

Equus caballus.

Key Location/Qualifiers

FT CDS 1.582 /tag= a

FT /product= "Equine IL-18"

OS W09956775-A1.

PD 11-NOV-1999.

PF 04-MAY-1999; 99WO-EP03098.

PR 07-MAY-1998; 98EP-0201451.

PA (ALKU) AKZO NOBEL NV.

PI Nicolson L, RiJke EO;

DR WPI; 2000-072212/06.

DR P-PSDB; Y58241.

PT Novel vaccine adjuvant used to increase the immune response

PS Claim 11; Page 22; 28pp; English.

XX This sequence represents cDNA encoding equine interleukin-18 (IL-18).
XX The cDNA was produced from alveolar macrophage mRNA via reverse
XX transcription using primer 255625, and the cDNA amplified via PCR using
XX primers 255626-255629. The invention relates to the use of recombinant
XX IL-18 as a vaccine adjuvant. Adjuvants are used in vaccines to
XX potentiate the immune response to an antigen derived from the pathogen.
XX It is important that the correct type of immune reaction is triggered,

CC since many types of immune mechanisms that can be activated are
CC inadequate for the control of a particular pathogen. Mice were injected
CC intramuscularly with a vaccine formulation either containing inactivated
CC pseudorabies virus (PRV) plus tetanus toxoid (TT), or a formulation
CC containing inactivated PRV, TT and 0.1 micrograms of recombinant murine
CC IL-18. When subsequently challenged with virulent PRV, unvaccinated
CC control mice all succumbed to the infection, and only 30% of mice
CC vaccinated with vaccine antigen alone (inactivated PRV plus TT) survived
CC the infection. In contrast, mice which received the same amount of
CC vaccine antigen in conjunction with IL-18 had an 80% survival rate
CC after infection. IL-18 may be used as an adjuvant in vaccines for the
CC immunisation of humans and other animals, such as pigs, sheep, birds,
CC cattle, dogs, horses and fish. An adjuvant composition comprising
CC IL-18 may be administered concomitantly or sequentially with a vaccine
CC formulation. Additionally, IL-18 nucleotides operably linked to
CC transcriptional regulatory sequences may be used in DNA vaccines for the
CC in vivo expression of IL-18 in the cells of a vaccinated animal.

Sequence 582 BP; 200 A; 102 C; 113 G; 167 T; 0 other;

Query Match 57.0%; Score 268.4; DB 21; Length 582;
Best Local Similarity 76.5%; Pred. No. 8.8e-67;
Matches 355; Conservative 1; Mismatches 102; Indels 6; Gaps 2;

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Oy 2 ACTTTGGCGGACTTCACTGTACACCGAGTAATACGAAATTAATGACCAAGTCTCT 61
Db 110 actttggcgaggttgaactaaactcacaatcagaatttgacgacgaagttcct 169
Oy 62 TCGTTGACAAAGA--CAGCTGTGTTGAGGATATGACTATTTGATCAAAAGTGCA 118
Db 170 tcaataaccaggaagaaatacaacctgtgttgagagataatcgtctcgtatgatacagaca 229
Oy 119 GTGAACCCAGACGACGATATATACATGTACAAAGACAGTGAAGAACAGACGTCG 178
Db 230 acgcaccccaagccagcagatattacatataatgataaagatgacctcactagaggtctag 289
Oy 179 CTGTGACCCCTCTCTGTGAAGATAGTAAAYGCTACCTCTCTGTAGAACAGATCA 238
Db 290 cgttaacctctcgtgagagtgagaaacgtctcactcctccgtaagaacaaatla 349
Oy 239 TTTCTTTGAGGAATGATCCACCTGAAATATTGATGATATACAAAGTATCTCATAT 298
Db 350 tttcctttaaagaaatgagtcctcctcgtgaataatgaagaatgacatcata 409
Oy 299 TCTTTCAGAAAGCTGTTCAGGAC--ACAACAAGATGAGTGTGATGATCTGATG 355
Db 410 tcttcagagaagtggtccagagacatgataagatacagtttgagttcttcacgtata 469
Oy 356 AAGGACACTTCTGCTGCCAAAGAAAGATGATGCTTCAACTCTGAAAAAAG 415
Db 470 aaggatacttctcagctgtgaaaaagagaatgacatcttcaaacatcatttgaagaaga 529
Oy 416 AGGATGAATGCGGATTAATCTGTAATGTTCTACTCTCACTCAATAC 459
Db 530 aggatgaaaaatgggataaatctgtcaatcgttcaacgttcaaac 573
```

RESULT 13

A10526 standard; cDNA; 477 BP.

A10526;

23-JUN-2000 (first entry)

Human Interleukin-18 (IL-18) nucleotide sequence.

Interleukin-18; production; IL-18; human; ss; medical injection product.

Homo sapiens.

~CN1243130-A.

stable than the corresponding wild type interferon-gamma inducing factor. The mutant IGFs are also claimed to enhance killer cell cytotoxicity and/or induce killer cell formation, and may therefore be useful as antitumour agents, antitumour immunotherapeutics, antiviral agents and antimicrobial agents. The mutant IGFs are also claimed to be useful for treating hepatitis, acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and thrombopenia caused by radiation and chemo-therapy.

Sequence 471 BP; 166 A; 78 C; 87 G; 140 T; 0 other:

XX
SQ

Query Match 52.6%; Score 247.8; DB 19; Length 471;
Best Local Similarity 73.3%; Pred. No. 5.4e-61;
Matches 344; Conservative 1; Mismatches 118; Indels 6; Gaps 2;

OY 2 ACTTTGGCCGACTTCACATCGTACAAACCCGAGTAATFCGGAATAATAATGCCAAGTTCTCT 61
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 2 acttttggaagacttggaaatctaataattacgcatagaagaatttgatgaccagttcct 61
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 62 TCGTTGACAAAAGACA--GCCTGTGTTGAGAGATATGACTGATATGTGATCAAAAGTGCCA 118
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 62 tcataggaccaagaagaatcgccctatttggaaatatgactgatcttcgactgtagagata 121
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 119 GTGAACCCCGACACCAGATGATTAATATCATGTATACAAAGCAGTGAAGTAAGACGACTGG 178
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 122 atgcacccccgacacattatlaaglatglaaaaagataagccagcctagagglatgg 181
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 179 CTGTGACCCCTCTGTGTGAAGATAGTAATAAAYGTATACCCCTCTCCTGTAAAGAACAAGATCA 238
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 182 ctgtaaatcatctctgtgtaagtcgtggaagaattccaacctctcccgtygaagacaataa 241
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 239 TTTCCTTTGAGCAAAATGAGATCCACCTGAAAAATTATGATGATATFACAAAGTAGTCTCATAT 298
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 242 ttccctttaaggaaatgatactcctcctgtaaacatcaagatatcaaaaaagtgcattcatat 301
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 299 TCTTTCAAAACGTTGTTCCAGSAC---ACAACAAGATGGAGTTTAATCTTTCACGTATG 355
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 302 tccttcagaagaagtgctcccaagacatgataaagaatgcaatttgatcttcacatcacg 361
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 356 AAGGACACTTCTTGCTGCGCAAAGAAGATGATGCTTTCAAACTCATTTGAAAAANA 415
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 362 aagataacttctcagcttgtgaaaaagagagagacccctlttaactcatlgtgaaaaaag 421
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 416 AGGATGAATAATGGGATPAAATCTGTAAATGTTCACTCTCACATAACTTACA 464
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 422 aggaatgaattggggagatgataatcaatgcttcacgttccaagaaga 470

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Page 12

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Total number of hits satisfying chosen parameters: 524120

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Post-processing: Minimum Match 0%
Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	470.6	99.9	471	4	US-08-908-005A-1
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4	247.4	52.5	579	3	US-08-896-501A-5
5	247.4	52.5	1120	5	US-08-884-324-2
6	127.8	27.1	1164	5	US-08-884-324-13
7	127.8	27.1	28994	5	US-08-884-324-14
8	122	25.9	2167	5	US-08-884-324-7
9	75.6	16.1	134	5	US-08-884-324-4
10	51.4	10.9	135	5	US-08-884-324-3
11	38.4	7.8	7218	1	US-08-332-463-14
12	36.8	7.2	4731	1	US-08-488-706-2
13	36.8	7.8	4731	5	US-08-772-270A-9
14	34.4	7.3	10614	1	US-08-135-511-35
15	34.4	7.3	10614	2	US-08-187-453-35
16	33.8	7.2	8920	2	US-08-446-855A-1
17	33.2	7.0	4467	2	US-08-565-907A-1
18	33.2	7.0	4467	4	US-08-910-551B-1
19	33.2	7.0	4467	4	US-08-909-425A-1
20	32.6	6.9	4821	1	US-08-053-614-3
21	32.6	6.9	4821	2	US-08-316-397B-3
22	32.6	6.9	4821	3	US-09-034-306-3
23	32.4	6.9	1326	6	PCT-US93-09782-3
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33	29.8	6.3	5035	2	US-08-616-392C-3	Sequence 3, Appl
34	29.6	6.3	26700	2	US-08-472-217-1	Sequence 1, Appl
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37	29.2	6.2	1600	5	US-09-028-819-14	Sequence 14, Appl
38	29.2	6.2	5033	1	US-08-038-768A-1	Sequence 1, Appl
39	29	6.2	3515	3	US-08-391-743A-1	Sequence 1, Appl
40	28.8	6.1	1837	4	US-08-909-965C-10	Sequence 10, Appl
41	28.8	6.1	2295	5	US-08-375-300-3	Sequence 3, Appl
42	28.8	6.1	2295	5	US-09-177-431-3	Sequence 3, Appl
43	28.8	6.1	2295	6	PCT-US95-16930-3	Sequence 3, Appl
44	28.8	6.1	3634	5	US-09-166-186-1	Sequence 1, Appl
45	28.8	6.1	3792	4	US-08-992-334-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-502-535B-1
Sequence 1, Application US/08502535B
Patent No. 5912324
GENERAL INFORMATION:
APPLICANT: OKAMURA, Haruki
APPLICANT: TANIMOTO, Tadao
APPLICANT: TORIGOE, Kakui
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: IEN-BETA PRODUCTION INDUCING PROTEIN AND
TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502.535B
FILING DATE: 14-JUL-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184162/1994
FILING DATE: 14-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 45057/1995
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKAMURA-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-377-3528
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..471
OTHER INFORMATION: /note= Xaa in position 70 is Met or Thr
US-08-502-535B-1

Query Match 99.9%; Score 470.6; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 2,4e-132;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCTGGCCGACTCTGATGATCAACCCGACGATACGGAATATAAGCAAGTCTC 60
DB 1 AACCTGGCCGACTCTGATGATCAACCCGACGATACGGAATATAAGCAAGTCTC 60
QY 61 TTCGTTGACAAAGACAGCCTGTGTCGAGATGATGATGATGATGATGATGATG 120
DB 61 TTCGTTGACAAAGACAGCCTGTGTCGAGATGATGATGATGATGATGATGATG 120
QY 121 GAACCCAGACAGAGATGATGATGATGATGATGATGATGATGATGATGATG 180
DB 121 GAACCCAGACAGAGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 181 GTGACCTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 181 GTGACCTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 241 TCCCTTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 300
DB 241 TCCCTTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 300
QY 301 TTTCGAAACGCTGTCGAGACACACAGATGATGATGATGATGATGATGATG 360
DB 301 TTTCGAAACGCTGTCGAGACACACAGATGATGATGATGATGATGATGATG 360
QY 361 CACTTCTGCTGTCGCAAAAGAGATGATGATGATGATGATGATGATGATGAT 420
DB 361 CACTTCTGCTGTCGCAAAAGAGATGATGATGATGATGATGATGATGATGAT 420
QY 421 GAAATGGGATTAATCTGTAATGTTCACTCTCACTAATCAATCAAGT 471
DB 421 GAAATGGGATTAATCTGTAATGTTCACTCTCACTAATCAATCAAGT 471

RESULT 2
US-08-908-005A-1
Sequence 1, Application US/08908005A
Patent No. 5914253

GENERAL INFORMATION:

APPLICANT: OKAMURA, Haruki
APPLICANT: TANIMOTO, Tadao
APPLICANT: TORIGOE, Kakuji
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: IN-BETA PRODUCTION INDUCING PROTEIN AND
NUMBER OF SEQUENCES: 9
TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,005A
FILING DATE: 11-AUG-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/502,535
FILING DATE: 14-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184162/1994
FILING DATE: 14-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 45057/1995
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROMDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKAMURA-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..471
OTHER INFORMATION: /note= Xaa in position 70 is Met or Thr
US-08-908-005A-1

Query Match 99.9%; Score 470.6; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 2,4e-132;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCTGGCCGACTCTGATGATCAACCCGACGATACGGAATATAAGCAAGTCTC 60
DB 1 AACCTGGCCGACTCTGATGATCAACCCGACGATACGGAATATAAGCAAGTCTC 60
QY 61 TTCGTTGACAAAGACAGCCTGTGTCGAGATGATGATGATGATGATGATGATG 120
DB 61 TTCGTTGACAAAGACAGCCTGTGTCGAGATGATGATGATGATGATGATGATG 120
QY 121 GAACCCAGACAGAGATGATGATGATGATGATGATGATGATGATGATGATG 180
DB 121 GAACCCAGACAGAGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 181 GTGACCTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 181 GTGACCTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 241 TCCCTTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 300
DB 241 TCCCTTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 300
QY 301 TTTCGAAACGCTGTCGAGACACACAGATGATGATGATGATGATGATGATG 360
DB 301 TTTCGAAACGCTGTCGAGACACACAGATGATGATGATGATGATGATGATG 360
QY 361 CACTTCTGCTGTCGCAAAAGAGATGATGATGATGATGATGATGATGATGAT 420
DB 361 CACTTCTGCTGTCGCAAAAGAGATGATGATGATGATGATGATGATGATGAT 420
QY 421 GAAATGGGATTAATCTGTAATGTTCACTCTCACTAATCAATCAAGT 471
DB 421 GAAATGGGATTAATCTGTAATGTTCACTCTCACTAATCAATCAAGT 471

RESULT 3
US-08-896-605A-7

Sequence 7, Application US/08896605A
Patent No. 5879942
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,605A
FILING DATE: 18 July 1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 207,691/1996
FILING DATE: 19-JUL-1996
PRIOR APPLICATION NUMBER: JP 156,062/1997
APPLICATION NUMBER: JP 156,062/1997
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: leader peptide
LOCATION: 1..108
IDENTIFICATION METHOD: S
NAME/KEY: mat peptide
LOCATION: 109..579
IDENTIFICATION METHOD: S
US-08-896-605A-7

Query Match 52.5%; Score 247.4; DB 3; Length 579;
Best Local Similarity 73.1%; Pred. No. 2,4e-65;
Matches 343; Conservative 2; Mismatches 118; Indels 6; Gaps 2;

DB 2 ACTTTGGCCACTTCACTGACCAACCCAGTAATACGATATATAAGACCAAGTTCTCT 61
110 ACTTTGGCAGCTGTAATTAATATACATCAAGAAATTTGAAGACCAAGTTCTCT 169
62 TCGTTGACAAGACA---GCGTGTGTCAGAGATGACTGATGATCAAGTCCCA 118
170 TCATTTGACAGAGAAATCGGCTCTATTGAGATGACTGATGCTGATGATGATA 229
119 GTGACCCCAAGACAGCTGATATATACATGTAACAAGACAGTGAAGAGAGACTGG 178
230 ATGCACCCCGACCATTTATTAAGTATGATAAAGATAGCCACCTGAGAGGTATGG 289
179 CTGAGACCTCTCTGTGAAGATAGTAAGATGCTACCTCTCTGTAAGACAGATCA 238
290 CTGTACTATCTCTGTGAAGTGTGAGAAATTTCAATCTCTCTGTGAGAGACAAATTA 349
239 TTTCCTTTGAGAAATGATCCACCTGAAATAATTTGATGATATACAAAGTATCTCATAT 298

DB 350 TTTCCTTTAAGGAAATGAATCCCTCGATTAACATCAAGATACAAAAGTACATCATAT 409
299 TCTTCAGAAAGCTGTCAGAC---ACAACAAGATGGATTTGATCTACTGATG 355
410 TCTTCAGAGAGAGTCCCGACGATGATATAGATGCAATTTGATCTCTCATACG 469
356 AAGACACTTCTTCTGTCGCAAGAGAGATGATCTTCAACATCATCTGAAAAAA 415
470 AAGCATCTTTTACCTTTGAGAAAGAGAGACCTTTTAAACATCATTTGAAAAAG 529
416 AGCATGAAATGGGATTAATCTGTAATGTTCACTCTCACTACTACTTACA 464
530 AGCATGATTTGGGATAGATCTATATGTTCACTGTTCAAAAGAGA 578

RESULT 4
US-08-896-501A-5
Sequence 5, Application US/08896501A
Patent No. 5891663
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996
PRIOR APPLICATION NUMBER: JP 31,474/1997
APPLICATION NUMBER: JP 31,474/1997
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: leader peptide
LOCATION: 1..108
IDENTIFICATION METHOD: S
NAME/KEY: mat peptide
LOCATION: 109..579
IDENTIFICATION METHOD: S
US-08-896-501A-5

Query Match 52.5%; Score 247.4; DB 3; Length 579;
Best Local Similarity 73.1%; Pred. No. 2,4e-65;
Matches 343; Conservative 2; Mismatches 118; Indels 6; Gaps 2;

```

LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: No
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: liver
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..177
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 178..283
IDENTIFICATION METHOD: S
NAME/KEY: mat peptide
LOCATION: 286..756
IDENTIFICATION METHOD: S
NAME/KEY: 3'UTR
LOCATION: 757..1120
IDENTIFICATION METHOD: E
US-08-884-324-2

Query Match      52.5%; Score 247.4; DB: 5; Length 1120;
Best Local Similarity 73.1%; Pred. No. 3.2e-65;
Matches 343; Conservative 2; Mismatches 118; Indels 6; Gaps 2

2 ACCTTGCCGCGATCTCAGTACCAACCCAGATAATACGGATATTAATGACCAGTTCTCT 61
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
387 AGCTTCGCAGCATCTGACATATTAAATTTAATTCATTAAGAATTTGAATTTGACCAAGTTCTT 346

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Query Match	Similarity	Score	247.4	DB 5	Length	1120	
Best Local	Similarity	73.1%	Pred. No. 3,2e-65				
Matches	343	Conservative	2	Mismatches	118	Indels	6
							Gaps
QY	2	ACTTTGGCCGACTTCTACTGTACTACACCCGAGTAATACGGAATATTAATGACCAAGTCTCT	61				
DB	287	ACTTTGGCCGAGCTGTGATCTAATTAATATGAGTCATAAAGAAATTTGAATGACCAAGTCTCT	346				
QY	62	TGCTTGACAAAAGACA--GCCTGTGTCGAGAGATATGACTGATATTTGATCAAAAGTCCCA	118				
DB	347	TCATATGACCAAGAAATGCGCCTCAATTTGGAAGATATGACGATTCGACTGTAGAGATA	406				
QY	119	GTGACCCCGAGACCAGCTGATATATATCATGTATACAAAGACGTGAAGTAAAGGACTGG	178				
DB	407	ATGCACCCCGAGACCAATTTATTAATAGATATGTATAAAGATAGCCACCTGAGAGATAG	466				
QY	179	CTGAGACCCCTCTGTGGAAGATAGTAATAAAGTCAACCTCCTCTGTAAAGACAAGTCA	238				
DB	467	CTGTAACTATCTCTGTGAAGTGTGAAAAATTTTCAATCTCTCTGTGAGACAAATTA	526				
QY	239	TTTCCTTTGAGAAATGATGATCCACCTGAAAAATTTGATGATATACAAAGTATCTATAT	298				
DB	527	TTTCCTTTAAGAAATGAAATGAAATCTCTGTATTAATCAAGATACAAAGATGACATCATAT	586				
QY	299	TCCTTGAAAGACTGTTCAGAGAC--ACAAAGATAGGATTTGGATCTTCCTGATG	355				
DB	587	TCCTTGAGAAATGTGCCAGAGATGATATTAAGATCAATTTGAATCTTCATCATACG	646				
QY	356	AAGGACACTTTCTGCTTGCCAAAAGAGAAATGATGCTTTCAAACTATTTGAAAAAA	415				
DB	647	AAGGATCTTTGACTGTGTGA AAAAGAGAGACCTTTTAACCTCATTTTGGAAAAAG	706				
QY	416	AGGATGAAAATGGGGATTAATCTGTAATGTTTCACTCTCACTAACTTCA	464				
DB	707	AGGATGAAATGGGGATAGATCTATTAATGTTTCACTGTTCAAAAGCAAGAA	755				

RESULT: 6

US-08-884-324-13

Sequence 13, Application US/08884324

Patent No. 6060283

GENERAL INFORMATION:

APPLICANT: Takamori OKURA

APPLICANT: Kakui TORIOE

APPLICANT: Masahi KURIMOTO

TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE

TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-


```

IDENTIFICATION METHOD: E
US-08-884-324-13

Query Match          27.1% Score 127.8; DB 5; Length 11464;
Best Local Similarity 73.3%; Pred. No. 6,7e-29;
Matches 178; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

OY 225 TAAGACAAAGATCATTTCTCTTGAGGAAATGATCCACCTGAAATATTGATGATATACA 284
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 11200 TTAGTATATGTTTTTTTCTCATAGAAATGATATCCTCTGTATACATCAAGATACAA 11259

OY 285 AAGTATCATATTCCTTCAGAAACGTTGCCAGAC---ACAAAGATGAGATTGA 341
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11260 AAGTACATCATATTCCTTCAGAGAGTGTCCTCCAGACATGTAATTAAGATGCAATTTGA 11319

OY 342 ATCTCACTGATGAGACACTTTCCTTGCTTGCCAAAGAGATGATGCTTCAACT 401
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11320 ATCTCATCATACGAGAGATTACTTCTAGCTTGTAAGAGAGAGACACTTTAAACT 11379

OY 402 CATTTGAAAAAAGATGAATGGGATTAATCTGTAATGTTCACTCTACTACTT 461
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11380 CATTTGAAAAAAGAGATGATTTGGGGATAGATCTAATATGTTCACTGTTCAAAAGCA 11439

OY 462 ACA 464
      |||
Db 11440 AGA 11442

RESULT 7
US-08-884-324-14
Sequence 14, Application US/08884324
Patent No. 6060283
GENERAL INFORMATION:
APPLICANT: Takanori OKURA
APPLICANT: Kakuji TORIGOE
APPLICANT: Masahiko KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 28994 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA

```

ORIGINAL SOURCE:

ORGANISM: human

TISSUE TYPE: placenta

FEATURE:

NAME/KEY: 5'UTR

LOCATION: 1..15606

IDENTIFICATION METHOD: E

NAME/KEY: leader peptide

LOCATION: 15607..15685

IDENTIFICATION METHOD: S

NAME/KEY: Inttron

LOCATION: 15686..17056

IDENTIFICATION METHOD: E

NAME/KEY: leader peptide

LOCATION: 17057..17068

IDENTIFICATION METHOD: S

NAME/KEY: Inttron

LOCATION: 17069..20451

IDENTIFICATION METHOD: E

NAME/KEY: leader peptide

LOCATION: 20452..20468

IDENTIFICATION METHOD: S

NAME/KEY: mat peptide

LOCATION: 20469..20586

IDENTIFICATION METHOD: S

NAME/KEY: Inttron

LOCATION: 20587..21920

IDENTIFICATION METHOD: E

NAME/KEY: mat peptide

LOCATION: 21921..22054

IDENTIFICATION METHOD: S

NAME/KEY: Inttron

LOCATION: 22055..26827

IDENTIFICATION METHOD: E

NAME/KEY: mat peptide

LOCATION: 26828..27046

IDENTIFICATION METHOD: S

NAME/KEY: 3'UTR

LOCATION: 27047..28994

IDENTIFICATION METHOD: E

US-08-884-324-14

Query Match 27.1%; Score 127.8; DB 5; Length 28994;

Best Local Similarity 73.3%; Pred. No. 1e-28;

Matches 178; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 225 TAAGAAACATCTCTTCTTGGAATGATCCACTGAAATATGATATACA 284

DB 26803 TTAGGTATGTTTTTCTCTATGAAATGATCTCTCTGATPACATCAAGATACAA 26862

QY 285 AAGGATCTCATCTTCTTTCGAACCTGTTCCAGAC---ACAACAAGATGGGTTTGA 341

DB 26863 AAGGATCTCATCTTCTTTCGAACCTGTTCCAGACATGATATTAAGATGCAATTTGA 26922

QY 342 ATCTTCACTGATGAAGACCTTCTTCTTCTGCAAAAGAGATATGCTTTCAACT 401

DB 26923 ATCTTCACTGATGAAGACCTTCTTCTTCTGCAAAAGAGATATGCTTTCAACT 26982

QY 402 CATCTGAAAAAAGATGAAATGGGATAAATCTGATGTTCACTCTCACTTA 461

DB 26983 CATCTGAAAAAAGATGAAATGGGATAAATCTGATGTTCACTCTCTCACTTA 27042

QY 462 ACA 464

DB 27043 AGA 27045

RESULT 8

US-08-884-324-7

Sequence 7, Application US/08884324

Patent No. 6060283

GENERAL INFORMATION:

APPLICANT: Takano, OKURA

APPLICANT: Kakui TORIOE

APPLICANT: Masahiro KURIMOTO

TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE

TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESS: BROWDY AND NETMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

Zip: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/884,324

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 185,305/96

FILING DATE: 27-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: OKURA-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 2167 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

ORIGINAL SOURCE:

ORGANISM: human

TISSUE TYPE: placenta

FEATURE:

NAME/KEY: exon + 3'UTR

LOCATION: 1..2167

IDENTIFICATION METHOD: E

US-08-884-324-7

Query Match 25.9%; Score 122; DB 5; Length 2167;

Best Local Similarity 75.7%; Pred. No. 1.8e-27;

Matches 165; Conservative 0; Mismatches 50; Indels 3; Gaps 1;

QY 250 GAATGATCCACCTCGAAATATTTATGATATACAAAGTATCTTCTTCAGAA 309

DB 1 GAAATGAATCTCCGAAATATTTATGATATACAAAGTATCTTCTTCAGAA 60

QY 310 CGGTGCCAGGAC---ACAACAAGATGAGTTGAATCTTCACTGATGAAGACACTT 366

DB 61 AGGTGCCAGGACATGATATTAAGATGATTTGAATCTTCACTGATGAAGACACTT 120

QY 367 CTGTGTCGCAAAAGAGATGATGCTTTCAAACTCATTTGAAAAAAGATGAAT 426

DB 121 CTAGCTTGAAAAAGAGAGACCTTTTAACTCATTTGAAAAAAGAGATGAATG 180

QY 427 GGGATTAATCTGATGTTCACTCTCACTACTTACA 464

DB 181 GGGATTAATCTGATGTTCACTCTCACTACTTACA 218

RESULT 9

US-08-884-324-4

Sequence 4, Application US/08884324

APPLICANT: Takamori OKURA
 APPLICANT: Kakui TORIGOE
 APPLICANT: Masahi KURIMOTO
 TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
 TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/884,324
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 185,305/96
 FILING DATE: 27-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: OKURA-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 135 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 ORIGINAL SOURCE:
 ORGANISM: human
 TISSUE TYPE: placenta
 FEATURE:
 NAME/KEY: exon
 LOCATION: 1..135
 IDENTIFICATION METHOD: S
 US-08-884-324-3

Query Match 10.9% Score 51.4; DB 5; Length 135;
 Best Local Similarity 70.9%; Pred. No. 8.2e-07;
 Matches 83; Conservative 0; Mismatches 31; Indels 3; Gaps 1

QY 2 ACTTTGGCCGACTCTACATGTACACCGCAGTAAATACGAAATTAATGACCAAGTTCTCT 61
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 19 ACTTTGGCAGCGTTAAATCTAAATATATCATGCTATAGAAATTTGATGATGACCAAGTTCTCT 78
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 62 TCGTTGACAAAGACA---GCCGTGTTGCGAGGATATGACTATATTTGATCAAAAGTG 115
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 Db 79 TCAATGACCAAGAAATCGCCCTCTATTGTAAGATATGACTGATTTCTGACTGTAGAG 135
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RESULT 11.
 US-08-232-463-14/c
 : Sequence 14, Application US/08232463
 : Patent No. 5670367
 : GENERAL INFORMATION:
 APPLICANT: DORNER, F.
 APPLICANT: SCHEIFLINGER, F.
 APPLICANT: FALKNER, F. G.
 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F15
US-08-232-463-14

Query Match 8.2%; Score 38.4; DB 1; Length 7218;
Best Local Similarity 8.1%; Pred. No. 0.036;
Matches 36; Conservative 207; Mismatches 203; Indels 0; Gaps 0;
QY 11 GACTTACTGTACACCGCAGTATACGGAATATAATGACCAAGTCTCTCGTTGACA 70
DB 1492 GGCATCTACTGATATCTATCTATGCAAGTAAAGAGATGAAGATTGTGACR 1433
QY 71 AAGACACGCTGTCTGAGATATGATGATCAAGTGCACGAGTGAACCCACA 130
DB 1432 RRR 1373
QY 131 CCACTGATATATACATGTACAAGACAGTAAAGAGACGCGTGTGACCTCT 190
DB 1372 RRR 1313
QY 191 CTGGAAGTAGTAAAGTCTACCTCTCTGTAAGAACAAGATCATTTCTTTGAGG 250
DB 1312 RRR 1253
QY 251 AATGATCCACCTGAATAATGATGATATACAAAGTCTCATATCTTTCACAAGC 310
DB 1252 RRR 1193
QY 311 GTGTTCCAGACACACAAGATGAGTTGAATCTTCACTGATGAAGACACTTTCTTG 370
DB 1192 RRR 1133
QY 371 CTGCAAAAGAGATGATCTTCAACTCATTTGAAAAAAGAGATGAATGAGG 430
DB 1132 RRR 1073
QY 431 ATAATCTGTAATGTCTACTCTCACT 456

DB 1072 RRRRRATCCAGCTCCTCGACT 1047
RESULT 12
US-08-488-706-2
Sequence 2, Application US/08488706
Patent No. 5994525
GENERAL INFORMATION:
APPLICANT: Kamp, Elbarte M.
APPLICANT: Smits, Marinus A.
TITLE OF INVENTION: Recombinant Vaccine for Prevention and/or
TITLE OF INVENTION: Treatment of Pleuropneumonia Infections
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Adelman, Freyne & Schwab
STREET: 708 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM PC or compatible
OPERATING SYSTEM: DOS 3.31
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,706
FILING DATE: 09-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/722,971
FILING DATE: 28-JUNE-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cihamon, Jay S.
REGISTRATION NUMBER: 24,156
REFERENCE/DOCKET NUMBER: 201,875
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-949-9190
TELEFAX: 212-949-9022
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4731
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-488-706-2
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Best Local Similarity 47.4%; Pred. No. 0.091;
Matches 110; Conservative 0; Mismatches 122; Indels 0; Gaps 0;
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DB 591 TCTATCTAGCAAAAAGATGACTGAAAATCATATATTTAAAGGAGGAAAATACAA 650
QY 271 ATTGATGATATACAAAGTCAATCTTCTTTCAGAAAGTGTCTCCAGGACACAACAG 330
DB 651 AAAAGTAGCTGAAGACATTTCTTTCAGTATGAGCAAGATTAATACAGCTCTCAAT 710
QY 331 ATGAGTTGATCTTCACTGATATGAGGACACTTTCTTCTGCCCCAAAAGAGATGAT 390
DB 711 AATATCTTAATGATCATATATTAAGAGAGACTTTTATGTCAAAAATCACTTGTG 770
QY 391 GCTTCAATCATTTGAAAAAAGAGATGAATGAGGATTAATGTTAA 442
DB 771 ATCATTAAATGCTCTTACACAAGATGAAAAAAGGAAAAACAAGTTA 822
RESULT 13
US-08-772-270A-9
Sequence 9, Application US/08772270A
Patent No. 6019984

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//08/135,511
FILING DATE: 13-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18748/175
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 10614 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-135-511-35.

Query Match      7.3%   Score 34.4: DB 1: Length 10614:
Best Local Similarity 46.6%: Pred. No. 0.68:
Matches 110: Conservative 0: Mismatches 126: Indels 0: Gaps 0

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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  10250 AACCTTAGCAAGACCTTGGAGGCATGATTACTTTGGAATATTTTGGAGTTTCTTGCAACA 10191

OY  289 GATCATCATTTCTTTCAAGAAGTGTTCCAGCACACAACAGATGAGITTTGAATCTTCA 348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  10190 AATCGATAAATATTTTAACTTACTCATGCGATGATGAATATAACATTTCTAAAGGTAA 10131

OY  349 CTGTATGAAGGACACTTTCTTGCTTGCCAAAAGAGAAGATGATGCTTCAAACACTATCTG 408
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  10130 AAGCACAAAATGTTCTTATTTTCATTTCTGAAAGGTAGGTAAATTTTAAAGTTACTGGTTT 10071

OY  409 AAAAAAAGGATGAANAATGGGATTAATCTGTAATGTTTACCCTCTCACTAACCTTACA 464
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Db  10070 AAAAATTTACTTATATTGTTAGTATAAGATPAAAGATPAAATATATTTTACATATA 10015

RESULT 15
US-08-187-453-35/C
Sequence 35, Application US/08187453
Patent No. 5753431
GENERAL INFORMATION:
APPLICANT: Chiang, John
TITLE OF INVENTION: Cholesterol 7a-Hydroxylase Gene
TITLE OF INVENTION: Regulatory Elements and Transcription Factors
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,453
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,488
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,510
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18748/188
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 10614 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-187-453-35

Query Match 7.3%; Score 34.4; DB 2; Length 10614;
Best Local Similarity 46.6%; Pred. No. 0.68;
Matches 110; Conservative 0; Mismatches 126; Indels 0; Gaps 0;
QY 229 AACAGATCATTTCTTTGAGCAATGATCCAGCTGAATATTTGATGATATACAAAGT 288
DB 10250 AACCTTACGAAAGCCTTTGAGTCAGATTAATTGAAATATTTTGGAGTTTCTTGAACA 10191
QY 289 GATCTCATATCTTTTCAGAAAGCTGTTCCAGACACACAGATGAGATTGAATCTTCA 348
DB 10190 AATCAGATAAATTAATTTTAATTATCAGTGAATGAATTAACATTTCTATTCAAAGTTA 10131
QY 349 CTGATGAGAGACACTTTCTTGCCTGCCAAGAGAGATGATGCTTTCAACTCAITCTG 408
DB 10130 AAGCACAATGTTCTTTTCAATTTCTGAAGGTAGTAATTTTAAAGTTACTGGTTT 10071
QY 409 AAAAAAAGATGAAATGGGATTAATCTGTAATGTTCTACTCTCACTTAATTACA 464
DB 10070 AAATATATTACTTATTAATTTGATATAGATAAAGATAATATAATTTACATATA 10015

Search completed: November 21, 2000, 21:30:35
Job time: 15082 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2000, 16:55:18 ; Search time 399.28 Seconds
(without alignments)
7293.383 Million cell updates/sec

Title: US-09-050-249-1

Perfect score: 471

Sequence: 1 AACCTGGCCGACTCCTG.....TCACACTTACATCAAGT 471

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapept 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3	355.6	77.6	512	20	AA125102	AA125102 EST1-M-BH2.
4	337.6	71.7	474	8	AI121020	AI121020 ud69c02.x
5	308.6	65.5	434	2	AA23736	AA23736 md69c01.r
6	274	58.2	469	10	AI463705	AI463705 vB8905.x
7	260.8	55.9	423	23	AA558748	AA558748 I0298E02
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11	197.4	41.9	342	13	AI835755	AI835755 UI-M-A10-
12	191.6	40.7	335	12	AA066410	AA066410 AV066410
13	173.4	36.8	289	2	AA245600	AA245600 mx30a01.r
14	166.8	35.4	505	8	AI104615	AI104615 ud69c02.y
15	155.6	33.0	574	19	AY597985	AY597985 AY597985
16	153.8	32.7	294	15	AV072353	AV072353 AY072353
17	153.8	33.7	354	12	AI642457	AI642457 vB80D10.x
18	153.4	33.6	292	15	AV065007	AV065007 AV063007
19	151.6	32.2	287	15	AV065008	AV065008 AV065008
20	148.4	31.5	276	15	AV078115	AV078115 AV078115
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24	139.4	29.6	300	17	AV139413	AV139413 AV239413
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28	130.4	27.7	279	15	AV087765	AV087765 AV087765
29	124.8	26.5	281	15	AV062592	AV062592 AV062592
30	117.2	24.9	259	15	AM338525	AM338525 xw80b03.x
31	114	24.2	549	20	AI180047	AI180047 xw80b03.x
32	92	19.5	515	13	AI800476	AI800476 xF69b11.x
33	78	16.6	655	96	AQ377384	AQ377384 tJ14hd05.x
34	63.8	13.5	325	20	AA142292	AA142292 EST292531
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36	56.6	12.0	168	8	AI129421	AI129421 qC38g11.x
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40	47.6	10.1	438	9	AV069285	AV069285 AV069285
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42	39.6	8.4	413	99	AA129391	AA129391 zN85D03.s
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45	37.4	7.9	751	23	AA687654	AA687654 NF011G05R

LOCUS	AA930362	603 bp	mRNA	EST	23-APR-1998
DEFINITION	vs53f07.r1 Scratagene mouse skin (#937311) Mus musculus cDNA clone IMAGE:1150597 5' similar to gb:A09949 Mouse mRNA for IGF precursor polypeptide (MOUSE); , mRNA sequence.				
ACCESSION	AA930362				
VERSION	AA930362.1	GI:3079955			
KEYWORDS	EST.				
SOURCE	house mouse-				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 603)				
AUTHORS	Gairis,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubaque,T., Geisel,S., Kuwaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.				
TITLE	The WashU-HHMI Mouse EST Project				
JOURNAL	Unpublished (1996)				
COMMENT	Contact: Maria M/Mouse EST Project				
	WashU-Mur Mouse EST Project				

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:623805
Seq primer: -28m3 rev1 ET from Amersham
High quality sequence stop: 445.

FEATURES
SOURCE

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/organism="Mus musculus"
/strain="C57BL/6"
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/clone="IMAGE:1510597"
/clone_lib="Stratagene mouse skin (#937313)"
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/tissue_type="whole skin"
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/note="Organ: skin; Vector: plhiscript SK-; Site_1: ECORT
; Site_2: xhoI; Cloned unidirectionally. Primer: Oligo
dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTT 3'"

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BASE COUNT
ORIGIN

Query Match	98.9%;	Score 465.8;	DB 7;	Length 603;
Best Local Similarity	99.28;	Pred. No. 1e-115;		
Matches 467; Conservative	1;	Mismatches 3;	Indels 0;	Gaps 0;

Query Match

al Similarity	99.2%	Pred. NO. 1e-113,	
467; Conservative	1;	Mismatches	3; Indels
			0; Gaps
			0;

467; Conservative

99.2%; Pred. No. 1e-110, 1; Mismatches 3; Indels 0; Gaps 0;

0y 61 TTCGTTGCAAAAGACAGCCTGTGTGAGAGATATGCTATATTTGATCAAAATGGCACT 120
 |||||
 |||||
 Db 65 TTCGTTGCAAAAGACAGCCTGTGTGAGAGATATGCTATATTTGATCAAAATGGCACT 124
 |||||
 0y 121 GACCCCGACACGACCTGATATATATCATGTACACAAAGACGTAGTAAGAGACTGGCT 180
 |||||
 |||||
 Db 125 GACCCCGACACGACCTGATATATATCATGTACACAAAGACGTAGTAAGAGACTGGCT 184
 |||||
 0y 181 GTGACCTCTCTGTGAAGAGATGTAAAAYGTACCTCTCTCTGTAAAGCAAGATCATTT 240
 |||||
 |||||
 Db 185 GTGACCTCTCTGTGAAGAGATGTAAAATGTCACTCCTCTCTGTAAAGCAAGATCATTT 244
 |||||
 0y 241 TCCCTTGAGGAATGATATCCACCTGAAAATTTGATGATATACAAAGTGAATCTCATATTC 300

Db	245	TCCTTTGGGAAATGGATTCACCTGAAATATGATGATATACAAAGATCTCATTC	304		
QY	301	TTTCGAAAGCTGTTCACGACACAAACAAGATGAGTTTGAATCTTCACTGTATGAAGA	360		
Db	305	TTTCGAAAGCTGTTCACGACACAAACAAGATGAGTTTGAATCTTCACTGTATGAAGA	364		
QY	361	CACCTTCTTCTGTTCGCAAAAGAGATATGCTTTCAACATCATTTCTGAAAAAAGAT	420		
Db	365	CACCTTCTTCTGTTCGCAAAAGAGATATGCTTTCAACATCATTTCTGAAAAAAGAT	424		
QY	421	GAAATGGGATTAATCTGTATGTTCACTCTCACTAATCTTACATCAAGT	471		
Db	425	GAAATGGGATTAATCTGTATGTTCACTCTCACTAATCTTACATCAAGT	475		
RESULT	2	AA892285	646 bp mRNA	EST	25-JAN-1999
LOCUS	AA892285/c	ES1196088	Normalized rat kidney, Bento Soares Rattus sp. cDNA clone		
DEFINITION		RI1A060.3	end, mRNA sequence.		
ACCESSION		AA892285			
VERSION		AA892285.1	GI:3019164		
KEYWORDS		EST.			
SOURCE		Rattus sp.			
ORGANISM		Rattus sp.			
REFERENCE		1 (bases 1 to 646)			
AUTHORS		Lee, N.H., Glodet, A., Chandra, I., Mason, T.M., Quackenbush, J.,			
TITLE		Kerlavage, A.R. and Adams, M.D.			
JOURNAL		Rat Genome Project: Generation of a Rat EST (REEST) Catalog & Rat			
COMMENT		Gene Index			
		Unpublished (1998)			
		Contact: Lee, NH			
		ATCC			
		The Institute for Genomic Research			
		9712, Medical Center Drive, Rockville, MD 20850, USA			
		Tel: (301)-838-3529			
		Fax: (301)-838-0208			
		Email: nhlee@tigr.org			
		Seq primer: M13-21.			
FEATURES		Location/Qualifiers			
source		1..646			
		/organism="Rattus sp."			
		/db_xref="arcc (inhost):2017880"			
		/db_xref="taxon:10118"			
		/clone="RK1A060"			
		/clone_1db="Normalized rat kidney, Bento Soares"			
		/note="Organ: kidney; Vector: pT73Pac; Site_1: EcoRI;			
		Site_2: NotI"			
BASE COUNT		177 a 126 c 123 g 220 t			
ORIGIN					
Query Match		85.1%; Score 400.6; DB 7; Length 646;			
Best Local Similarity		91.8%; Pred. No. 4.4e-98;			
Matches 434; Conservative		1; Mismatches 35; Indels 3; Gaps 1;			
QY	2	ACTTGGCCGACTTACTGTTACACCGCAGTATACGGAATATTAATGACCAAGTTCTCT	61		
Db	579	ACTTGGCAGACTTCACTGTTACACCGCAGTATACGGAATATTAATGACCAAGTTCTCT	520		
QY	62	TGCTGACAAAAGA---CAGCCTGTGTTCGAGATATACATGATATGATCAAAATGGCA	118		
Db	519	TGCTGACAAAAGA---CAGCCTGTGTTCGAGATATACATGATATGATCAAAATGGCA	460		
QY	119	GTCGACCCGACGACGATGATATATACATGATATGATCAAAAGACGATGATGAGGACTGG	178		
Db	459	AGCATGCCAGACGACGATGATATATATGATGATGATGATGATGATGATGATGATGATG	400		
QY	179	CTGTGACCCCTCTCTGTGAGGATGATTAANAAGTCTTACCTCTCTGTGTAAGAACAAGATCA	238		

DB	Accession	Version	KeyWords	Source	Organism	Reference Authors Title	Journal MEDLINE COMMENT
Db	339	CTGGACCCCTTCTGTGAGAGATGGAAGAGTCTACCTCTCCTGTAAACAAACAAATCA					
QY	239	TTTCCTTTGAGGAATGATCCACCTGAAATATATGATATACAAAGTATCATAT					
Db	339	TTTCCTTTGAGGAATGATCCACCTGAAATATATGATATACAAAGTATCATAT					
QY	299	TCCTTCAGAAACGCTGTCAGGACACAAACAGATGAGATTGAAATCTTCACTGATGAAG					
Db	279	TCCTTCAGAAACGCTGTCAGGACACAAACAGATGAGATTGAAATCTTCACTGATGAAG					
QY	359	GACACTTCTTCGCTTGGCCAAAGGAGATGATGCTTCAACATCATCTGAGAAAAAGG					
Db	219	GACACTTCTTCGCTTGGCCAAAGGAGATGATGCTTCAACATCATCTGAGAAAAAGG					
QY	419	ATGAATATGGGATTAATCTGTAAATGTTCACTTCCTACTTAACATCAATCAAGT					
Db	159	ATGAATATGGGATTAATCTGTAAATGTTCACTTCCTACTTAACATCAATCAAGT					
RESULT	3	AM125102	512 bp	mRNA	EST	22-OCT-1999	
LOCUS		UI-M-BH2.1-8px-g-10-0-UI.s1					
DEFINITION		UI-M-BH2.1-8px-g-10-0-UI 3', mRNA sequence.					
ACCESSION		AM125102					
VERSION		AM125102.1	GI:6100632				
KEYWORDS		EST;					
SOURCE		house mouse.					
ORGANISM		Mus musculus					
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
AUTHORS		1 (bases 1 to 512)					
TITLE		Bonaldo,M.F., Lennon,G. and Soares,M.B.					
JOURNAL		Normalization and subtraction: two approaches to facilitate gene					
MEDLINE		discovery					
COMMENT		Genome Res. 6 (9), 791-806 (1996)					
		97044477					
		Contact: Chin, H					
		National Institute of Mental Health					
		6001 Executive Blvd. Room 7N-7150, MSC 9643, Bethesda, MD					
		20892-9643, USA					
		Tel: 301 443 1706					
		Fax: 301 443 9890					
		Email: mst@mail.nih.gov					
		The sequence contained an oligo-dT track that was present in the					
		oligonucleotide that was used to prime the synthesis of first					
		strand cDNA and therefore this may represent a bonafide poly A					
		tail. The sequence tag present in the cDNA between the NotI site					
		and the oligo-dT track served to identify it as a clone from the					
		normalized basal ganglia library cDNA library preparation: M.B.					
		Soares Lab Clone distribution: NIH BMAP cDNA clones will be made					
		available by the means that is soon to be determined. When NIH					
		determines the means for distribution of the BMAP cDNA clones, this					
		record will be updated accordingly when that means is determined.					
		The following repetitive elements were found in this cDNA sequence:					
		17-81, >MSTD#LIR/MaLR					
		Seq primer: M13 Forward					
		POLY-A-yes.					
FEATURES		Location/Qualifiers					
Source		1..512					
		/organism="Mus musculus"					
		/strain="C57BL/6J"					
		/db_xref="taxon:10090"					
		/clone="UI-M-BH2.1-8px-g-10-0-UI"					
		/clone_lib="NIH_BMAP_M.S3.1"					
		/dev_stage="27-32 days"					
		/lab_host="DH10B (Life Technologies)"					
		/note="vector: p773D-Pac (Pharmacia) with a modified					
		polylinker; site_1: Not I; site_2: Eco RI; The					
		NIH_BMAP_M.S3.1 library is a subtracted library of a					
		series ultimately derived from a mixture of individually					
		tagged normalized libraries from ten regions of the mouse					

Query Match	77.6%	Score 365.6	DB 20	Length 512
Best Local Similarity	99.7%	Pred. No. 1.2e-88		
Matches 365	Conservative	1	Mismatches 0	Indels 0
				Gaps 0
QY 106 GATCAAGTGGCCAGTGAACCCGACACGAGCTGATTAATATACATGTATACAAAGACGTGAA				165
Db 512 GATCAAAAGTGGCAGTGAACCCGACACGAGCTGATTAATATACATGTATACAAAGACGTGAA				453
QY 166 GTAGAAGAGACTGGCTGTGACCTCTCTGTGAAGATTAATAAAATCTACCTCCCTG				225
Db 452 GTAAAGAGACTGGCTGTGACCTCTCTGTGAAGATTAATAATCTACCTCTCCCTG				393
QY 226 AAGAACAAATCATTTCTCTTGAAGAAATGATTCACCTGAAATATTTGATGATATACAA				285
Db 392 AAGAACAAATCATTTCTCTTGAAGAAATGATTCACCTGAAATATTTGATGATATACAA				333
QY 286 AGTGATCTCATATTTCTTTGAGAAAGCTGTTCCAGAGCACAAACAATAGAGTTTAACT				345
Db 332 AGGATCTCATATTTCTTTGAGAAAGCTGTTCCAGAGCACAAACAATAGAGTTTAACT				273
QY 346 TCACGTATGAAGAGACACTTCTTGCTGCCAAAAGAGAGATGATGCTTCAACTCAT				405
Db 272 TCACGTATGAAGAGACACTTCTTGCTGCCAAAAGAGAGATGATGCTTCAACTCAT				213
QY 406 CTGAAAAAAAAGGATGAAAAATGGGGATAATCTGTAATGTACCTGCTACTACTACT				465
Db 212 CTGAAAAAAAAGGATGAAAAATGGGGATAATCTGTAATGTACCTGCTACTACTACT				153
QY 466 CAAAGT 471				
Db 152 CAAAGT 147				

RESULT 4

LOCUS A1121020/c

DEFINITION

u69602.x1 Sugano mouse, liver mla Mus musculus cDNA clone

IMAGE:1451138.3, similar to gb:D49949 Mouse mRNA for IGF precursor

ACCESSION A1121020

VERSION A1121020.1

KEYWORDS GI:3521344

SOURCE EST.

ORGANISM house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 474)

```

FEATURES
SOURCE
Location/Qualifiers
1..474
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone_image="1451138"
/clone_lib="Sugano mouse liver mlia"
/sex="Female"
/dev_stage="adult"
/lab_host="DHI08"
/note="Organ: liver; Vector: pME18s-FL3; Site_1: DraIII
(CACGTGTCG); Site_2: DraIII (GACCATGTG); 1st strand cDNA
was primed with an oligo (dT) primer
(AAGTCGCTTTTTTTTTTTTTT); double-stranded cDNA was
ligated to a DraIII adaptor (TGTGGGCTACTG), digested
and cloned into distinct DraIII sites of the pME18s-FL3
vector (5' site CACGTGTCG, 3' site GACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer GTTGTGCTCTTAAGCTGCG and 3' end
primer CGACGTGAGCTCGACACA."
132 a 97 c 83 g 162 t

```

Query Match	71.7%:	Score 337.6:	DB 8:	Length 474:
Best Local Similarity	99.7%:	Pred. Mismatches	0:	Gaps
Matches 337:	Conservative	1:	Indels	0:
QY 134	GACTGATATATATCATCTATCATGTACAAAGACAGTGAAGTAAAGAGACTGCGTGTGACCCCTCTCTG	193		
Db 474	GACTGATATATATCATGTACAAAGACAGTGAAGTAAAGAGACTGCGTGTGACCCCTCTCTG	415		
QY 194	TGAAGGATAGTAAATGCTTACCCCTCTCCGTGAAGAACAAAGATCATTTCTCTTGAGAGAA	253		
Db 414	TGAAGGATAGTAAATGCTTACCCCTCTCCGTGAAGAACAAAGATCATTTCTCTTGAGAGAA	355		
QY 254	TGATTCACCTGAAATATTTGATGATATACAAAGTATCTCATATTTCTTTGAGAAACGTG	313		
Db 354	TGATTCACCTGAAATATTTGATGATATACAAAGTATCTCATATTTCTTTGAGAAACGTG	295		
QY 314	TTCCAGGACACAAACAGATGGAGTTTGATCTTCTACCTGTATGAAAGACACTTTCTTGCTT	373		
Db 294	TTCCAGGACACAAACAGATGGAGTTTGATCTTCTACCTGTATGAAAGACACTTTCTTGCTT	255		
QY 374	GCCAAAGGAAGATGATGCTTTTCAAACCTCAATTCGAAAAAAGAGATGAATAATGGGATA	433		
Db 234	GCCAAAGGAAGATGATGCTTTTCAAACCTCAATTCGAAAAAAGAGATGAATAATGGGATA	175		
QY 434	AATCGTATATGTCACCTCTCACTAATCTTACATCAAACT	471		
Db 174	AATCGTATATGTCACCTCTCACTAATCTTACATCAAACT	137		

RESULT 5
LOCUS AA237736 434 bp mRNA EST 03-MAR-1997
DEFINITION mx23901.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:681648 5' similar to gb:D49949 Mouse mRNA for IGIF precursor polypeptide (MOUSE);, mRNA sequence.

ACCESSION AA237736
VERSION AA237736.1 GI:1861775
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 433)
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL: contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:421352
Putative full length read
vector to vector length is 437
Seq primer: -28ml3 rev2 ET from Amerham.
Location/Qualifiers
1. 434
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:681648"
/clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5']
TGTACCAATCTGAAGTGGAGCGCGGGAATCTTTTCTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. Library constructed and normalized by Bento Soares and M.Fatima Bernaldo."

BASE COUNT 139 a 79 c 92 g 124 t
ORIGIN

Query Match 65.5%; Score 308.6; DB 2; Length 434;
Best Local Similarity 99.7%; Pred. No. 3e-73;
Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 163 GAAGTAGAGAGCTGGCTGGACCCCTCTGTGAGAGTAGTAAGTACCCCTCC 222
Db 1 GAAGTAGAGAGCTGGCTGGACCCCTCTGTGAGAGTAGTAAGTACCCCTCC 60

QY 223 TGTAGAACAAGATCATTTCTTGGAGAAATGATCCACCTGAATATGATGATATA 282
Db 61 TGTAGAACAAGATCATTTCTTGGAGAAATGATCCACCTGAATATGATGATATA 120

QY 283 CAAAGTATCTCATATTTCTTCAAGAAAGTGTCCAGACACAACAAGATGAGATTGAA 342
Db 121 CAAAGTATCTCATATTTCTTCAAGAAAGTGTGTCCAGACACAACAAGATGAGATTGAA 180

QY 343 TCTTCACTGTATGAGACACCTTCTGCTGCCAAGAGAGATGATCTTCAACTC 402
Db 181 TCTTCACTGTATGAGACACCTTCTGCTGCCAAGAGAGATGATCTTCAACTC 240

QY 403 ATTCTGAAAAAAGATTAATAATGGGATTAATCTGATGTTCACTCTCACTACTA 462
Db 241 ATTCTGAAAAAAGATTAATAATGGGATTAATCTGATGTTCACTCTCACTACTA 300

QY 463 CATCAAGT 471
Db 301 CATCAAGT 309

RESULT 6
LOCUS AI463005/c 469 bp mRNA EST 09-MAR-1999
DEFINITION vb89g05.x1 Soares mouse 3NDMS Mus musculus cDNA clone IMAGE:764216 3' similar to gb:D49949 Mouse mRNA for IGIF precursor polypeptide (MOUSE);, mRNA sequence.

ACCESSION AI463005
VERSION AI463005.1 GI:4317035
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 469)
Marras, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Maria M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL: contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:465136
This clone was previously sequenced on the 5' end only, this new data is from the 3' end
High quality sequence stop: 324.
Location/Qualifiers
1. 469
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:764216"
/clone_lib="Soares mouse 3NDMS"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5']
TGTACCAATCTGAAGTGGAGCGCGGCTGTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bernaldo."

BASE COUNT 132 a 99 c 90 g 144 t
ORIGIN

Query Match 58.2%; Score 274; DB 10; Length 469;
Best Local Similarity 90.7%; Pred. No. 6.9e-64;

ethanol-precipitation. The cDNAs were ligated to
lone-linker L₁-Sal3 (include SalI sequence). The cDNAs
were purified by phenol/chloroform and separated from
free linkers by Centricon 100. Then, cDNAs were amplified
by long-range high fidelity PCR using Takara's Ex Taq
polymerase. Then, the cDNAs were purified by
phenol/chloroform and by Centricon 100. The cDNAs were
digested with SalI and NotI enzymes. Then, the cDNAs were
size selected by Gidco's Size Fractionation Column. The
cDNAs were cloned into SalI/NotI site of pSPORT plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by chemical method. The library was
constructed by Xiaohong Wang and Yulan Piao."

BASE COUNT 116 a 84 c 81 g 142 t

ORIGIN

Query Match 55.4%; Score 260.8; DB 23; Length 423;
Best Local Similarity 94.9%; Pred. No. 2.5e-60;
Matches 279; Conservative 1; Mismatches 13; Indels 1; Gaps 1;

Oy 179 CTGTGACCCCTCTGTGAAGATAGTAAAYGTCTACCTCTTCGTGTAAGAACAAGATCA 238
|||||
Db 423 CTGGACCCTCTCTGTGAAGATATAAATGTCTACCTCTCTGTAGACCAGATCA 364
|||||
Oy 239 TTTCCTTTGAGAAATGATGCACCTGAAAATATTGATGATATACAAATGATCATAT 298
|||||
Db 363 TTTCCTCTGTGAGAAATGATGCCACTCATAAATATTGATGATATACAAAGATCTCATAT 304
|||||
Oy 299 TCTTCAGAAACGCTTCCAGACACACAAAGATGAGATTTGAATCTTCACGTATGANG 358
|||||
Db 303 TCGATCAGAAACGCTTCCAGACACACAAAGATGAGATTTGAATCTTCACGTATGANG 244
|||||
Oy 359 GACACTTCTCTGCTTGCCAAAGAGATGATGCTTTTAAACCTATCTC-AAAAAAAG 417
|||||
Db 243 GACACTATCTAGCTTGCCAAAGAGATGATGCTATCAACTCATCTTGAAAAAAG 184
|||||
Oy 418 GATGAATATGGGATTAATCTGTATGTTCTACTCTCTACTACTTACATCAACAT 471
|||||
Db 183 GATTAATAATGGGATTAATCTGTATGTTTACTCTCTACTACTTACATCAATAGT 130
|||||

RESULT 8 EST 06-AUG-2000
AV597984/c 443 bp mRNA Bos taurus cDNA clone
LOCUS AV597984 Bos taurus cartilage fetus Bos taurus cDNA clone
DEFINITION EICRA035C10 3', mRNA sequence.
ACCESSION AV597984 GI:9715479
VERSION AV597984.1
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 443)
Sugimoto, Y., Hirotsune, S., Takasuga, A., Itoh, R., Jitohzono, A. and
Suzuki, H.
bovine cDNA sequencing
Unpublished (2000)
Contact: Yoshihazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Niimi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@ccoc.nic.ac.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
1..443
/organism="Bos taurus"
/db_xref="taxon:9913"

FEATURES
Source

Query Match	50.9%;	Score 239.8;	DB 19;	Length 443;
Best Local Similarity	75.5%;	Pred. No. 1.2e-54;		
Matches 324;	Conservative 1;	Mismatches 98;	Indels 6;	Gaps 2

RESULT 9
AM049334/c LOCUS AM049334 357 bp mRNA EST 18-SEP-1999
DEFINITION U1-M-BH1-amr-f.-09-0-U1.s1.N.H_EMAP_M.S2 Mus musculus cDNA clone
U1-M-BH1-amr-f.-09-0-U1.3 , MRNA sequence.
ACCESSION AM049334
VERSION AM049334.1 GI:5909863
KEYWORDS EST:
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 357)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL MEDLINE
CONTACT: Chin, H

Genome Res. 6 (9), 791-806 (1996)
97044477

Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bona fide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-*or* track served to identify it as a clone from the normalized brain stems library cDNA Library Preparation: M.B. Soares lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence

18-84, >MSTD#LIR/MaIR
Seq primer: M13 Forward
PolyA-yes.

FEATURES	Location/Qualifiers
source	1. .357

source

1. .357
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="01-M-BH1-amr-f-09-0-01"
/clone_id="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pYT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The
NIH_BMAP_M_S2 library is a subtracted library derived from
NIH_BMAP_M_S1, which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hippocampus). The driver
used for subtraction consisted of a pool of 5,000 clones
from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries.
TAG_Lib=NIH_BMAP_M_S2
TAG_TISSUE=brain-stems
TAG_SEQ=TCAATG"

Query Match	44.28;	Score 208;	DB 19;	Length 357;
Best Local Similarity	100.08;	Pred. No. 4.5e-46;		
Matches 208;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	264	TGAAATTTGTAGTATPACAAAATGATNTCATCTTTCTTCAGAAAGCTGTCCAGACA	323
Db	357	TGAAAAATTGTATATATACAAAGTGATCTCATAATTCTTCAGAAAGCTGTCCAGACA	298
OY	324	CACACAGATGAGATTGGATCTTCACTGTGTGAAGAAGCACCTTTCTTCTGCCAAAAGA	383
Db	297	CACACAGATGAGATTGGATCTTCACTGTGTGAAGAAGCACCTTTCTTCTGCCAAAAGA	298
OY	384	AGATGATGCTTTTCCAACATCATTTCTGAAAAAAAAAAGCATGAAAAATGGGATTAATCTGTAAT	443
Db	237	AGATGATGCTTTTCCAACATCATTTCTGAAAAAAAAAAGCATGAAAAATGGGATTAATCTGTAAT	178
OY	444	GTCACCTGCCTCACTAACCTTAACATCAAAG	471
Db	177	GTCACCTGCCTCACTAACCTTAACATCAAAG	150

RESULT	10			
AL1176343/c				
LOCUS	AL1176343	369 bp	mRNA	EST
DEFINITION	EST1219926	Normalized rat ovary,	Bento Soares	Rattus sp. cDNA clone
	ROV0838.3'	end, mRNA sequence.		
ACCESSION	AL1176343			
VERSION	AL1176343.1	GI:4134870		
KEYWORDS	EST.			
SOURCE	Rattus sp.			
ORGANISM	Rattus sp.			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

VERSION AV066410.1 GI:5186238
 EST.
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Mus musculus
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 335)
 AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Horii, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, T., Kikuchi, N., Kojima, Y., Matsuyama, T., Naitsumu, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomimaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 TITLE RIKEN Mouse ESTs
 JOURNAL Unpublished (1999)
 COMMENT Contact: Chie Owa
 Genome Science Laboratory
 RIKEN
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098
 Email: genome-res@cc.riken.go.jp
 Thermolabile and thermocyclization of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3435-3460 (1998))
 Please visit our web site (<http://genome.its.riken.go.jp>) for further details.
 FEATURES
 source location/Qualifiers
 1..335
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="2010109E01"
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 /tissue-type="small intestine"
 /dev-stage="adult"
 /dev_59_c 67 g 100 t
 BASE COUNT 109 a 59 c 67 g 100 t
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 Matches 197; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Oy 266 AAAATATTGATGATATACAAAGTGCATATCTTTCAGAAAGCTGTCAGACACA 325
 Db 1 AAAATATTGATGATATACAAAGTGCATATCTTTCAGAAAGCTGTCAGACACA 60
 Oy 336 ACAAGATGAGATTTGAATCTTCAGTATGAAGACACTTCTTCTGCCAAAGAG 385
 Db 61 ACAAGATGAGATTTGAATCTTCAGTATGAAGACACTTCTTCTGCCAAAGAG 120
 Oy 366 ATGATGCTTCAACTCATCTTGAAGAAAGGATGAAGATGAAGTGAATGT 445
 Db 121 ATGATGCTTCAACTCATCTTGAAGAAAGGATGAAGATGAAGTGAATGT 180
 Oy 446 TCACCTCCTCACTTACATCAAGT 471
 Db 181 TCACCTCCTCACTTACATCAAGT 206
 RESULT 13
 AA245600 289 bp mRNA EST 10-MAR-1997
 LOCUS mx30a01.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:661672 5'
 DEFINITION similar to gb:D49949 Mouse mRNA for IGIF precursor polypeptide (MOUSE);, mRNA sequence.
 ACCESSION AA245600

VERSION AA245600.1 GI:1876519
 EST.
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Mus musculus
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 289)
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheinberg, K., Steppe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wille, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@lmn1.riken.go.jp) for further information.
 MGI:421376
 Trace considered overall poor quality
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 1.
 FEATURES
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 1..289
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 /clone="IMAGE:661672"
 /clone_1lb="Soares mouse NML"
 /tissue-type="liver"
 /lab_host="DH10B"
 /note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCAATCATGAGTGGGCGGCGGCAATCTTTTCTTTTCTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 77 a 51 c 75 g 86 t
 ORIGIN
 Query Match 36.8%; Score 173.4; DB 2; Length 289;
 Best Local Similarity 79.2%; Pred. No. 9.5e-37;
 Matches 229; Conservative 1; Mismatches 57; Indels 2; Gaps 2;
 Oy 167 TAAGAGCATGCGCTGTACCTCTCTGTGAGGATAGTAATATCTACCTCTCCGTA 226
 Db 1 TAGTAGGACATGCTGTGTGCTGTGTGAGGATAGTAATATCTACCTCTCCGTA 60
 Oy 227 AGAAGATCATCTTCCT-TTGAGGAATGATGATGATGATGATGATGATGATGAT 285
 Db 61 AGAAGATCATCTTCCTTCAGTGAAGAAATGATGATGATGATGATGATGATGAT 120
 Oy 286 AGTATCTCATATCTTTCAGAAAGTGTTCAGAGACACAAGATGAGTCTTGA-ATC 344
 Db 121 AGTATCTCATATCTTTCAGAAAGTGTTCAGAGACACAAGATGAGTCTTGA-ATC 180
 Oy 345 TTCACGTATGAGACACTTCTTCTGCCAAAGAGATGATGCTTCAAGTAT 404
 Db 181 TGCCTCTGCTGCTGCTACCTTCTTCTGCCAAAGATGATGATGCTTCAAGTAT 240
 Oy 405 TCTGAAAAAAGATGAAATGGGATGAATCTGTAATGCTCCTC 453
 Db 241 TCTGACCAACAAGATGATGAGGATGATGATGATGATGATGATGATGATGATGAT 289

